

205210 9249660

1 GTCC TTCACCATG CACTCGCTGGGCTTCTCTCTGTGGCGTGTTCTCTCTGCTCGCCGCTG 60
-----+-----+-----+-----+-----+-----+-----+-----+
CAGGAAGGTGTACGTGAGCGACCCGAAAGAGACACCGCACAAAGAGACGAGCGGCGAC
M H S L G F F S V A C S L L A A A -
61 CGCTGCTCCCGGTCCTCGGAGGCGCCCGCCCGCCCGCCGCTTCGAGTCCGGACTCG 120
-----+-----+-----+-----+-----+-----+-----+-----+
GCGACGAGGCGCCAGGAGCGCTCCGGGGCGGGCGGGCGGAGCTCAGGCCCTGAGC
L L P G P R E A P A A A A F E S G L D -
121 ACCTCTCGGACGCGGAGCCCGACGCGGGCGGAGGCCCGCTTATGCAAGCAAAGATCTGG 180
-----+-----+-----+-----+-----+-----+-----+-----+
TGGAGAGCCCTGCGCCTCGGGCTCGGCCCGCTCCGGTGCCGAATACGTTCTGTTCTAGACC
L S D A E P D A G E A T A Y A S K D L E -
181 AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAAGTCACTGACTGTACTCTACCCAGAAT 240
-----+-----+-----+-----+-----+-----+-----+-----+
TCCTCGTCAATGCCAGACACAGGTCACATCTACTGTAGTACTGACATGAGATGGGTCTTA
E Q L R S V S S V D E L M T V L Y P E Y -
241 ATTGGAAATGTACAAGTGTGCTAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG 300
-----+-----+-----+-----+-----+-----+-----+-----+
TAACCTTTTACATGTTACAGTCGATTCCTTCTCCGACCGTTGTATTTGTTCTTGTCC
W K M Y K C Q L R K G G W Q H N R E Q A -
CCAACCTCAACTCAAGGACAGAGAGACTATAAAATTGCTGCAGCACATTATAATACAG

MATCH WITH FIG. 1B
FIG. 1A

360
GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATATGTC
N L N S R T E E T I K F A A A H Y N T E -
361
AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCAATGCCACGGGAGGTGT
TCTAGAACTTTTCAATAACTATTACTCACCTCTTCTGAGTTACGTACGGTGCCCTCCACA
I L K S I D N E W R K T Q C M P R E V C -
421
GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
CATATCTACACCCCTTCCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
I D V G K E F G V A T N T F F K P P C V -
541
TGTCCGTCTACAGATGTGGGGTTTGCTGCAATAGTGAGGGCTGCAGTGCATGAACACCA
ACAGGCAGATGTCTACACCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
S V Y R C G C C N S E G L Q C M N T S -
541
GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCAAGGCCCCA
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGATTCGGGGT
T S Y L S K T L F E I T V P L S Q G P K -
601
AACCAGTAACAATCAGTTTTCGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
TTGGTCAATTGTTAGTCAAAACGGTTAGTGTGAAGGACCGCTACGTACAGATTTGACCTAC
P V T I S F A N H T S C B C M S K L D V -
601

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

661 TTTACAGACAAGTTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGC 720

AAATGCTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGCACAG
Y R Q V H S I I R R S L P A T L P Q C Q -

721 AGGCAGCGAACAAGACCTGCCCCCAACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780

TCCGTCGCTTGTCTGGACGGGGTGAATGATACACCTTATTAGTGTAGACGCTACGG
A A N K T C P T N Y M W N H I C R C L -

781 TGGCTCAGGAAGATTTTATGTTTTCTCGGATGCTGGAGATGACTCAACAGATGGATTCC 840

ACCGAGTCCCTTCTAAAAATACAAAAGGAGCCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D S T D G F H -

841 ATGACATCTGTGGACCAACAAGGAGCTGGATGAAGAGACCTGTCTAGTGTCTGCAGAG 900

TACTGTAGACACCTGGTTGTTCCTCGACCTACTTCTCTGGACAGTCAACACAGACGCTCTC
D I C G P N K E L D E E T C Q C V C R A -

901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT 960

GCCCCGAGCCGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C -

961 GTGTCTGTAAAAACAACACTCTTCCCCAGCCAATGTGGGGCCCAACCGAGAATTGATGAAA 1020

CACAGACATTTTGTGAGAAGGGGTCGGTTACACCCCGGTGGCTCTTAAACTACTTT

MATCH WITH FIG. 1D FIG. 1C

2052TD-9249E000

4/47

MATCH WITH FIG. 1C

V	C	K	N	K	L	F	P	S	Q	C	G	A	N	R	E	F	D	E	N	-
ACACATGCCAGTGTGTATGTAAAGAACCCTGCCCCAGAAATCAACCCCTAAATCCTGGAA																				1080
TGTTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGATTAGGACCTT																				1021
T	C	Q	C	V	C	K	R	T	C	P	R	N	Q	P	L	N	P	G	K	-
AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC																				1140
TTACACGGACACTTACATGTCTTTTCAGGTGTCTTTACGAACAATTTTCTTCTTCAAGG																				1081
C	A	C	E	C	T	E	S	P	Q	K	C	L	K	G	K	K	F	H	-	
ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAGGCTTGTGAGC																				1141
TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG																				1200
H	Q	T	C	S	C	Y	R	R	P	C	T	N	R	Q	K	A	C	E	P	-
CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCTTCATATTTGGCAAAGACCAC																				1260
GTCCTAAAAGTATATCACTTCTTTCACACAGCAACACAGGGAAGTATAACCGTTTCTCGTG																				1201
G	F	S	Y	S	E	E	V	C	R	C	V	P	S	Y	W	Q	R	P	Q	-
AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAACTGTGT																				

MATCH WITH FIG. 1E FIG. 1D

MATCH WITH FIG. 1D

```

1261  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320
      TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
      M S
1321  TCCACAGTAGAACTGTCTGTGAACAGAGAGACCCCTTGTGGGTCCATGCTAACAAAGACA 1380
      ACGGTGTCATCTTGACAGACACTTGCTCTCTGGAACACCCAGGTACGATTGTTCTGT
      AAAGTCTGTCTTTCCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440
      TTTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC
      CAAAAGGCCCTCTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500
      GTTTCCGGAGAACATTCTGACCAAAGACGGTTACTGGTTTGTCTGGTTCTCTAAAAGGAG
      TTGTGATTTCTTAAAGAATGACTATATAATTTATTTCCACTAAAAATATTTGTTCTGTC
1501  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560
      AACACTAAAGAAATTTCTTACTGATATATAATAAAGGTGATTTTATATAACAAGACG
      ATTCATTTTATAGCAACAACAATTGGTAAACTCACTGTGATCAATATTTTATATCAT
1561  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620
      TAAGTAAAAATATCGTTGTTGTTAAACCATTTTGAGTGACACTAGTTATAAAATATAGTA
      GCAAAATATGTTTAAAAATAAAAATGAAAATTGTATTATTATAAAAAAAA
1621  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1674
      CGTTTTATACAAATTTTATTTTACTTTTAAACATAAATATTTT

```

FIG. 1E

209210 9249660

1 CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
71 AGATGAACATCATGACTGTACTCTACCCAGAATATTGGAAAATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAAGAC
-----+-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATATGAGTG
-----+-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
-----+-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTCTCCGTCTACAGATGTGGGGGTTGCTG
-----+-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C

FIG. 2A

```

361 CAATAGTGGGGCTGCAGTGCATGAACACCAGCAGCTACCTCAGCAAGACGTTATT
    N S E G L Q C M N T S T S Y L S K T L F

421 TGA AATTACAGTGCCTCTCTCTCAAGGCCCAACACAGTAACAATCAGTTTGGCCAATCA
    E I T V P L S Q G P K P V T I S F A N H

481 CACTTCCCTGCCGATGCTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
    T S C R C M S K L D V Y R Q V H S I I R

541 ACGTTCCTGCCAGCAACACTACCACAGTGTGAGCAGCGAACAAGACCTGCCCCACCAA
    R S L P A T L P Q C Q A A N K T C P T N

601 TTACATGTGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTTATGTTTCCTC
    Y M W N N H I C R C L A Q E D F M F S S

661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAAGAGCT
    D A G D D S T D G F H D I C G P N K E L

```

FIG. 2B

FIG. 2C


```

1081  TCGTTGTGCCCTTCATATTGGCAAGACCACAAATGAGCTAAGATTGTACTGTTTCCCA
      R C V P S Y W Q R P Q M S
1141  GTTCATCGATTCTTCTATTATGGAAAACTGTGTGTCACAGTAGAACTGCTGTGAACAGA
1201  GAGACCCTTGTGGTCCCATGCTAACAAAGACAAAAGTCTGCTTTCCTGAACCATGTGGA
1261  TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAGACTGGTTT
1321  CTGCCAATGACCAACAGCCAAGATTTCCTCTTGTGATTTCTTTAAAGAATGACTATA
1381  TAAATTATTTCCACTAAAAATATTGTTTCTGCAATTCATTTTATAGCAACAACAATTGGT
1441  AAACTCACTGTGATCAATAATTTTATATCATGCAGCAAAATATGTTTAAAAATGAAAA
1501  TTGTATTATAAAAAAAAAAAAAA

```

FIG. 2D

10/47

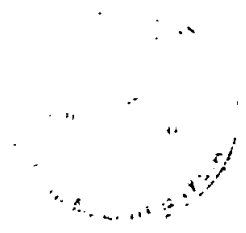
2020-09-09

1	50
Pdgfa	.MRTLACLLL LCGYLAHVL AEEAEPREV IERLARSQIH SIRDLORLLE
Pdgfb	MNRCWA.LFL SLCCYRLVS AEGDPIPEEL YEMLSHSIR SFDDLORLLH
VegfMNFL SWVHWSLALL LY.....LHHAKWSQA
Vegf2MTV LYPEYWKMYK CQ.....LRKGGWQH
51	100
Pdgfa	IDSVGSEDSL DTSRAHGVH ATKHVPEKRP LPIRRKRSI.EEAVP
Pdgfb	GDP.GEEDCA ELDLNMTRSH SGCELES... .LARGRRSLG SLTIAEPAMI
Vegf	APMAE.....GGCQ NHHEVWKFMD .VYQR.....
Vegf2	REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK.....
101	150
Pdgfa	AVCKTRTVIY EIPRSQVDPT SANFLIWPCC VEVKRCGTCC NTSSVKQPS
Pdgfb	AECKTRTEVF EISRRLLDRT NANFLVMPCC VEVQRCSCCC NNRNVQCRPT
Vegf	SYCHPIETLV DIFQEPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2	TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQMMNT
151	200
Pdgfa	RVHRSVKVA KVEYVRKKPK LKEVQVRLEE HLEQAC.... AT.....
Pdgfb	QVQLRPVQVR KIEIVRKKPI FKATVTLED HLAQCC.... ETVAAARPVT
Vegf	EESNITMQIM RIK.PH..QG OHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2	STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII

FIG. 3A

201		250
PdgfaTSLNPD YREEDTIVR.....	
PdgfbRSPGGSQEQR AKTPQTRVTI RTIVRVRPPK GKHKFKHTH DKTALKETLG	
VegfRGK.....GKGQRKRK KSRYKSWSVY VGARCCIMPW SLPGPHP...	
Vegf2	RRSLPATLPQ CQAANKTCPT NYMNNHICR CLAQEDFMFS SDAGDDSDTG	
251		300
Pdgfa	
Pdgfb	A.....	
VegfCGP.....CSE RRKHLFVQDP QTCKCCKNT	
Vegf2	FHDICGPNKE LDEETCCVC RAGLRPASCG PHKEL...DR NSCQCVCCKNK	
301		350
Pdgfa	
Pdgfb	
VegfDSRCKARQ LELNERTCRC DKPRR.....	
Vegf2	LFPSQCGANR EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPOKCLL	
351		398
Pdgfa	
Pdgfb	
Vegf	
Vegf2	KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRVCPS YWQRPQMS	

FIG. 3B



PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLOWING TABLE				
	PDGF α	PDGF β	VEGF	VEGF2
PDGF α				
PDGF β	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

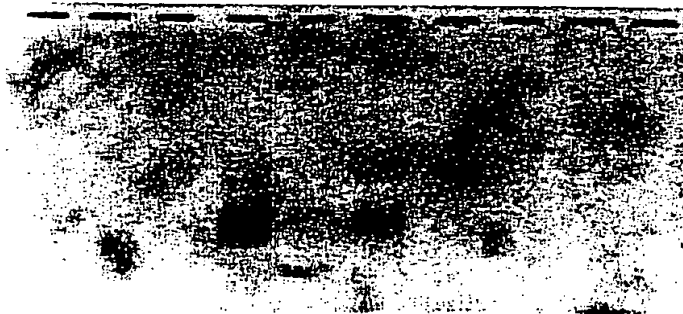
FIG.4

405470 945660

13/47

Expression of VEGF2 mRNA in
Human Breast Tumor Cells

1 2 3 4 5 6 7 8 9



◀ 28 S

◀ 18 S

Lane 1. normal breast tissue
Lane 2. breast tumor tissue
Lane 3-9. breast tumor cell lines.

FIG.5

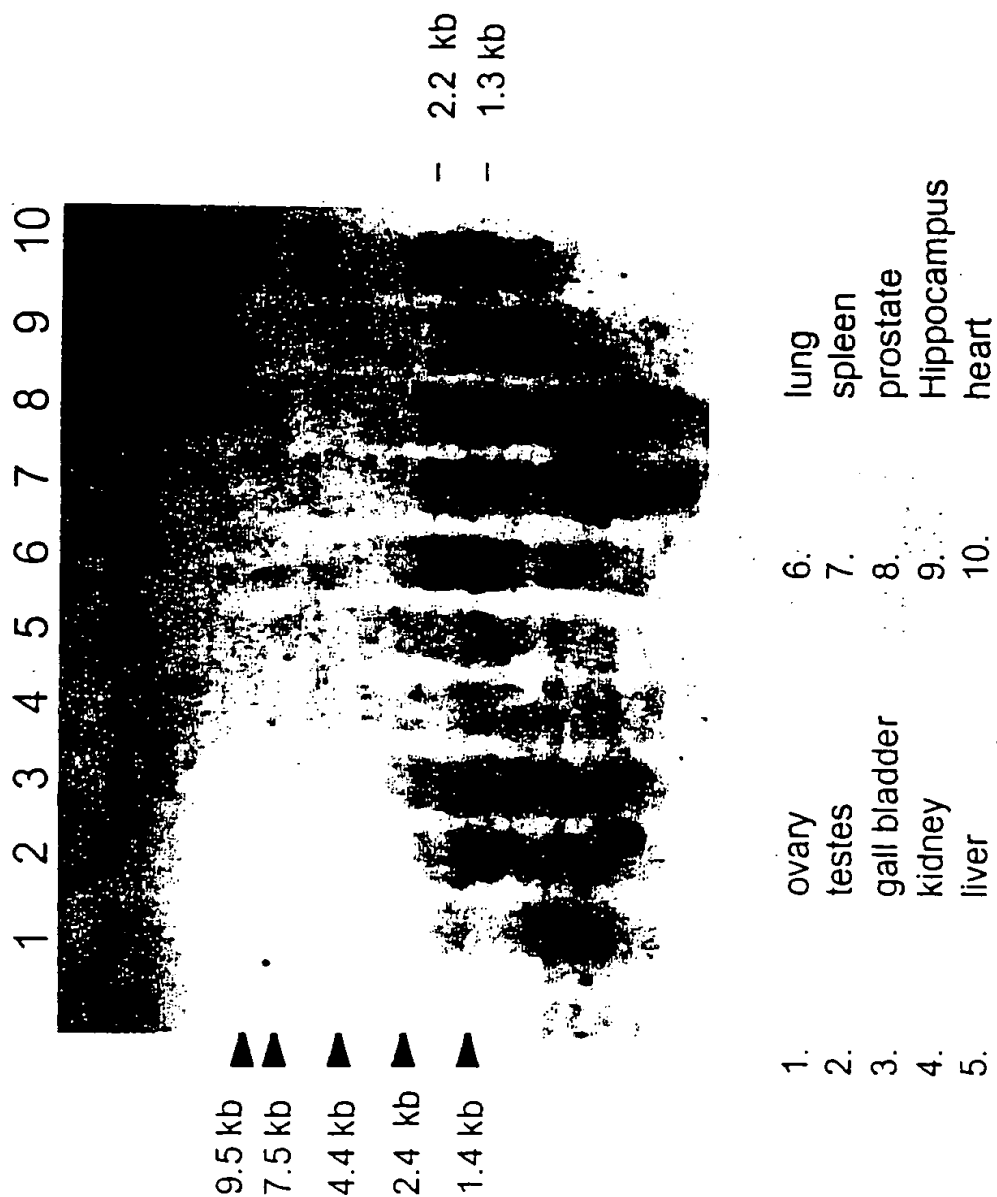
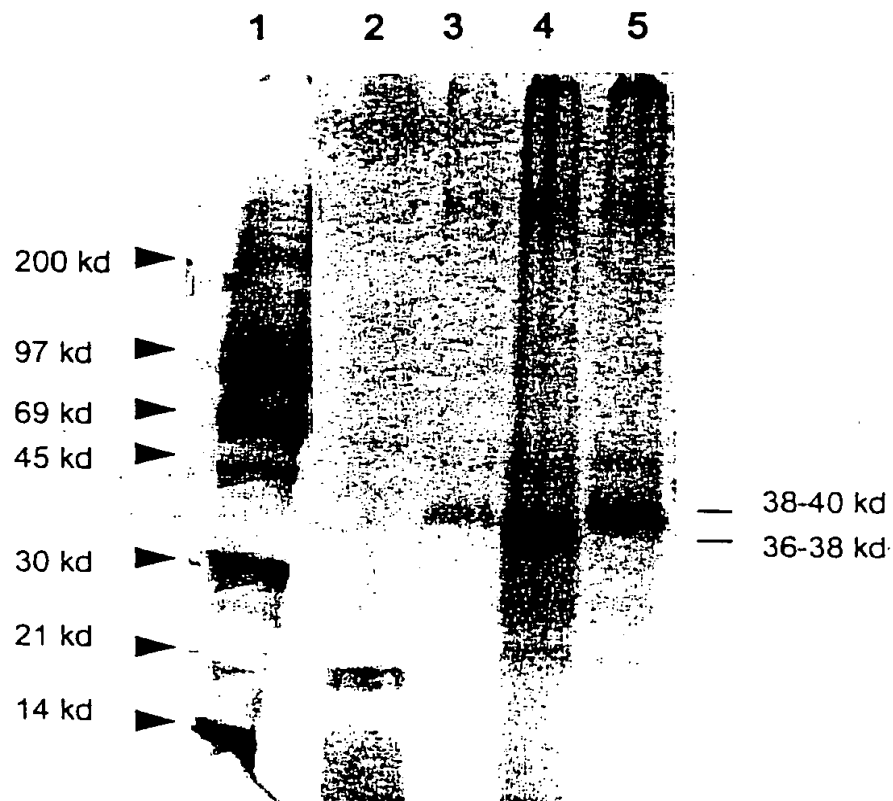


FIG.6

Expression of VEGF2 mRNA in human adult tissues.



- Lane 1: 14-C and rainbow M.W. marker
- Lane 2: FGF control
- Lane 3: VEGF2 (M13-reverse & forward primers)
- Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
- Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG.7

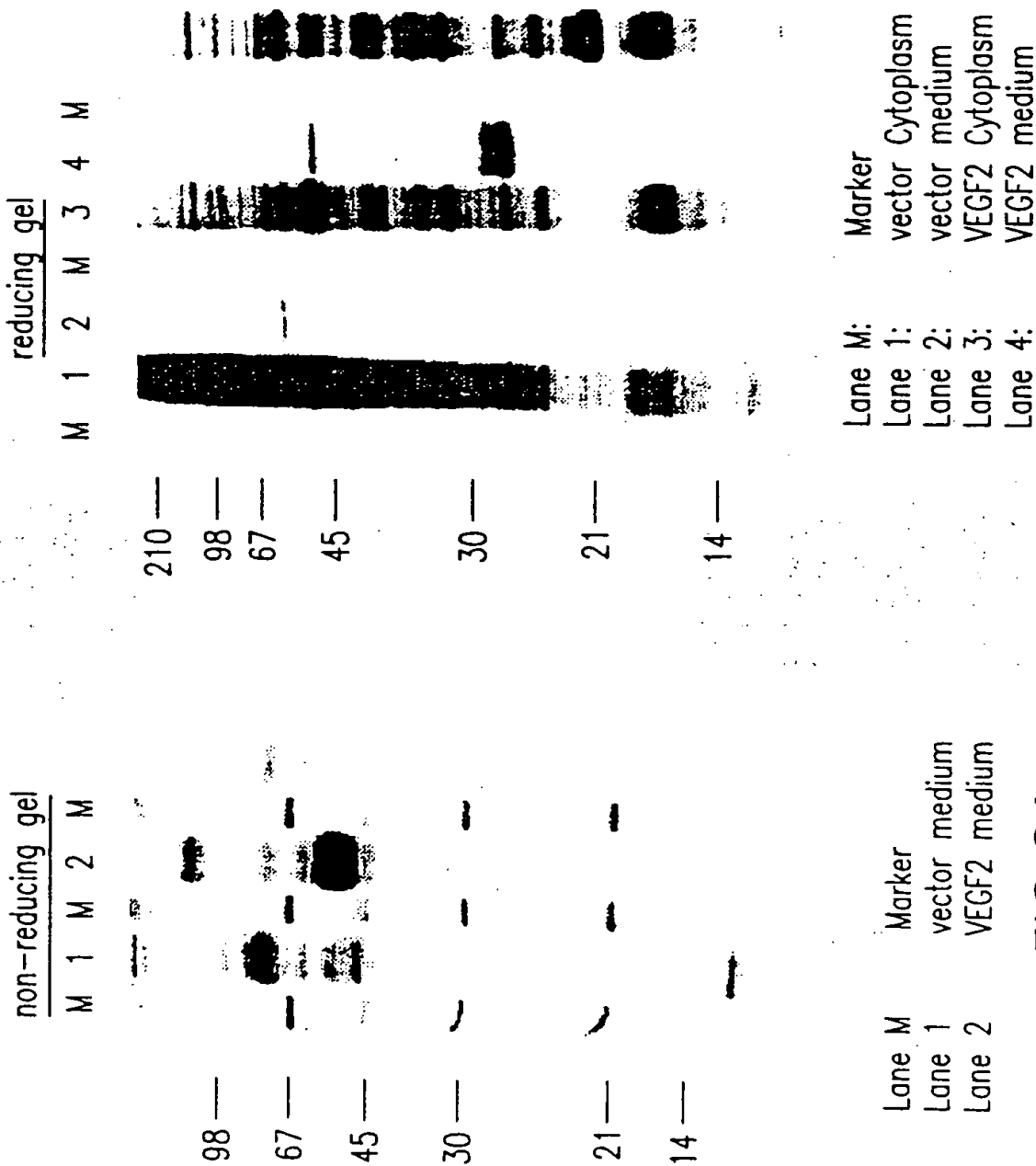
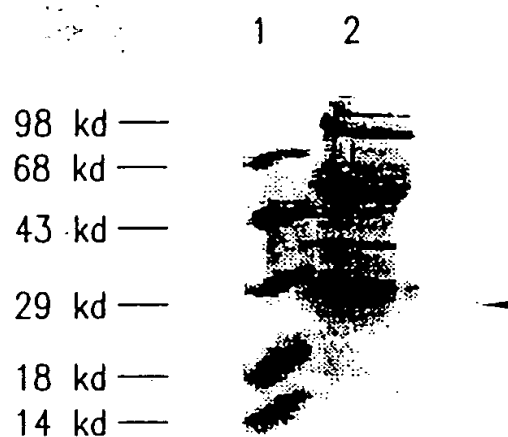


FIG. 8A

FIG. 8B

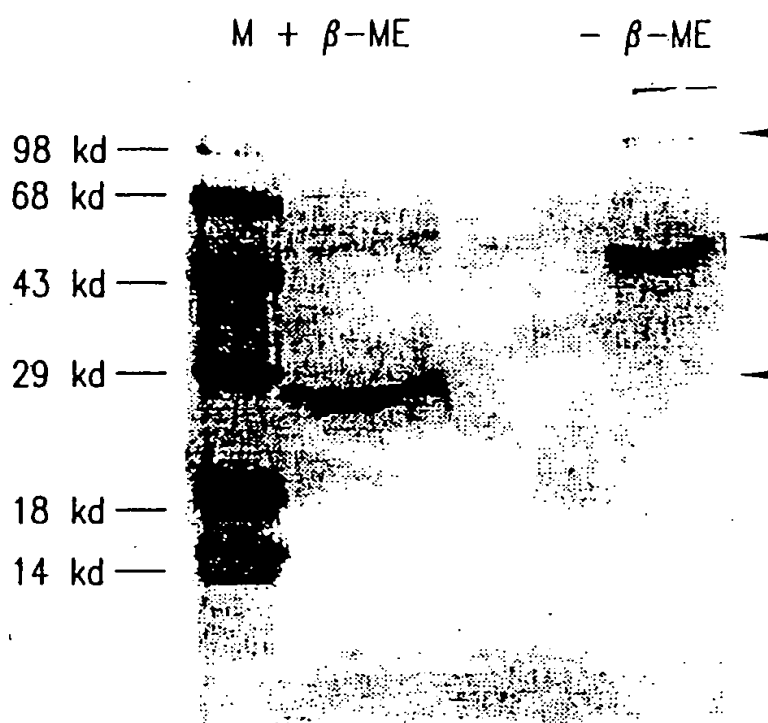
17/47

FIG.9



Lane 1: Molecular weight marker
Lane 2: Precipitates containing VEGF2.

FIG.10



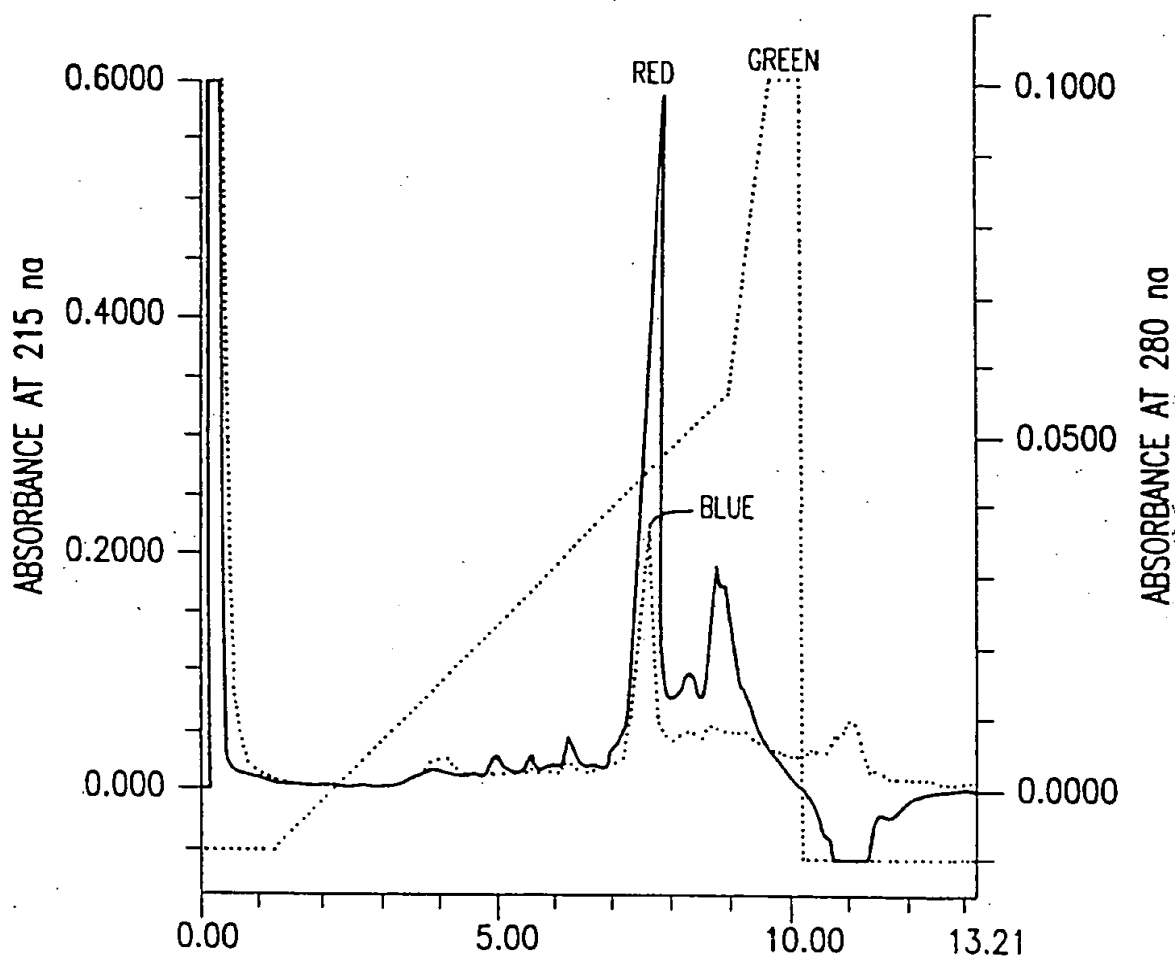


FIG. 11

FIG.12

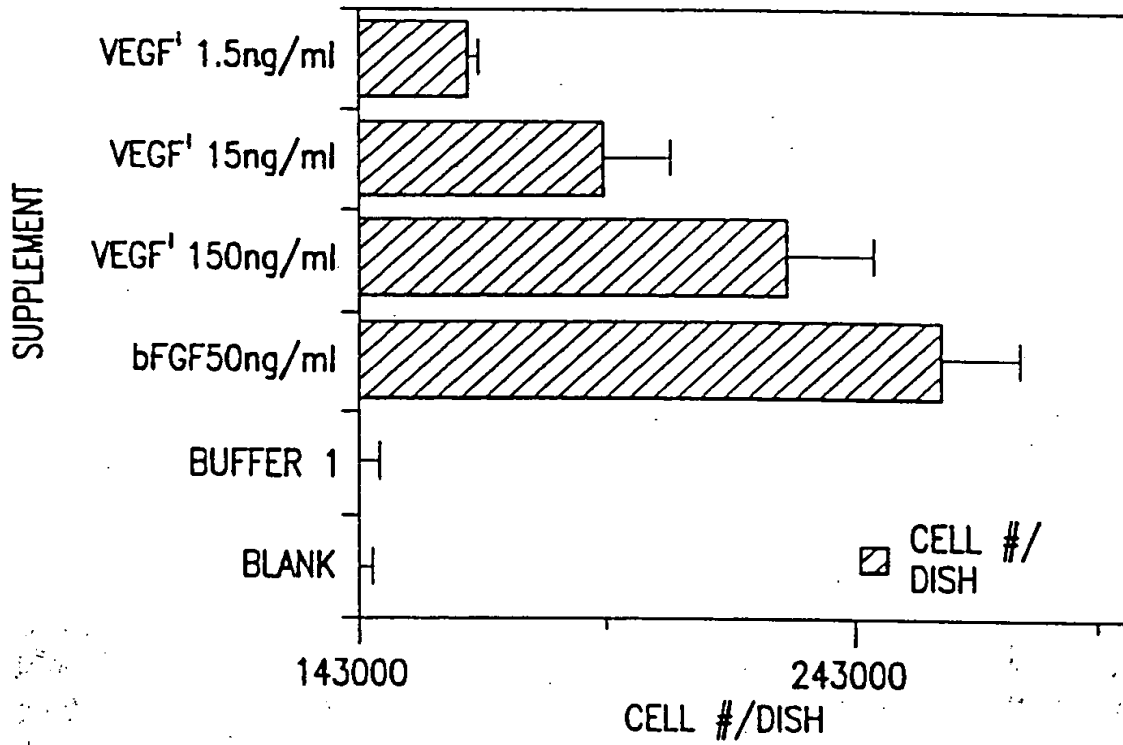


FIG.13

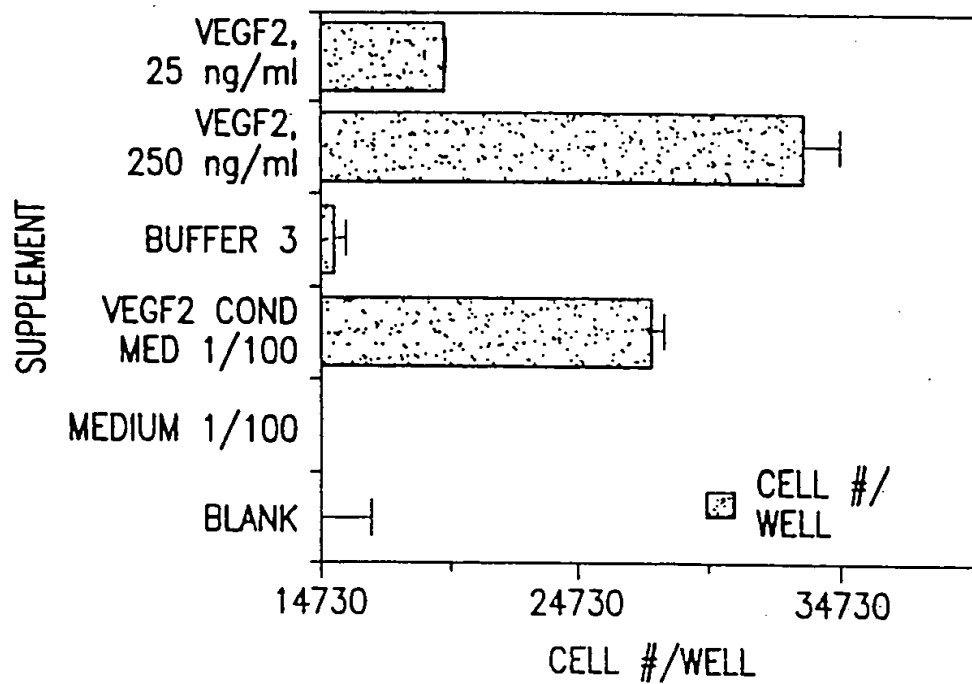


FIG.14A

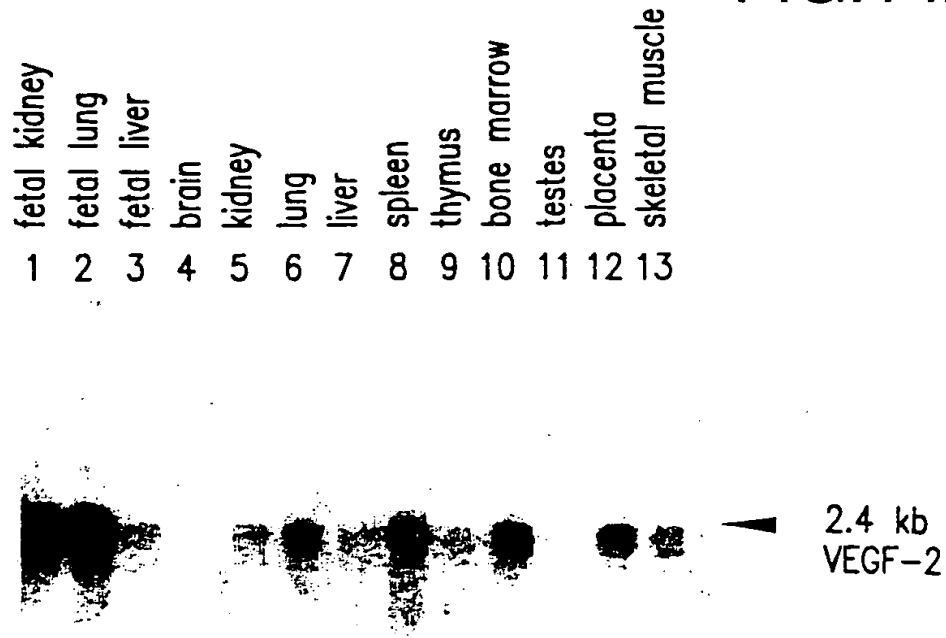
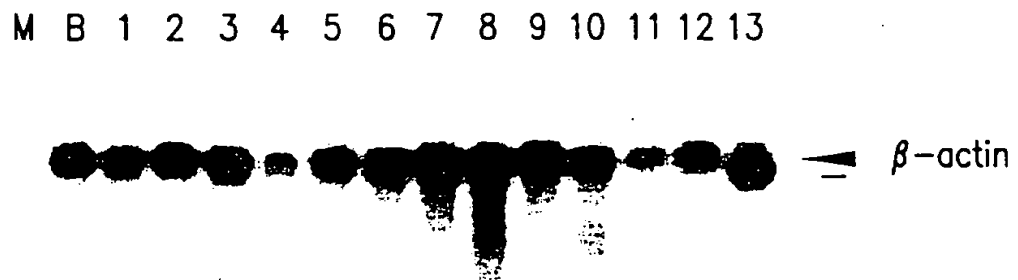
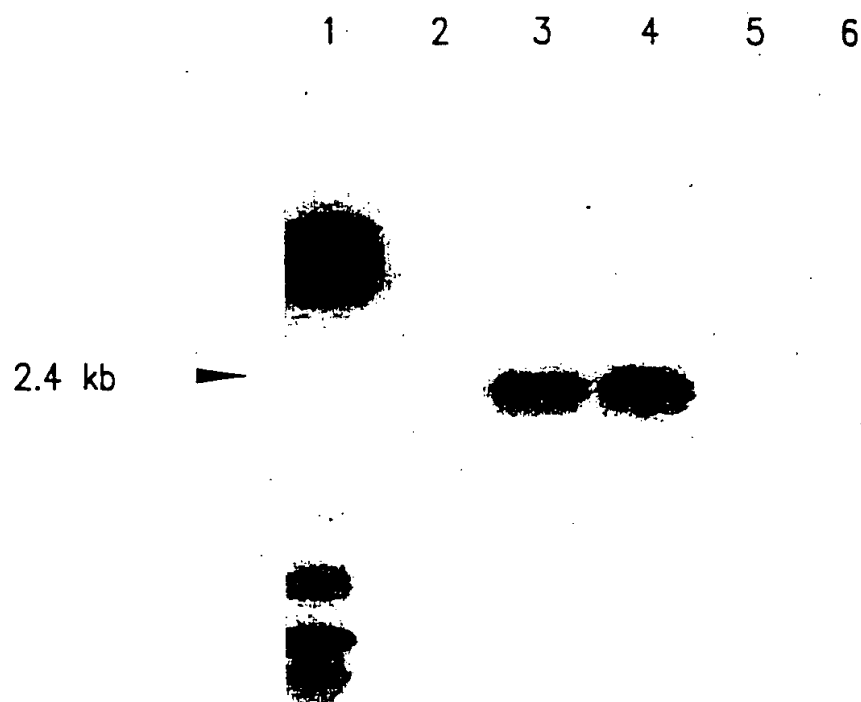


FIG.14B



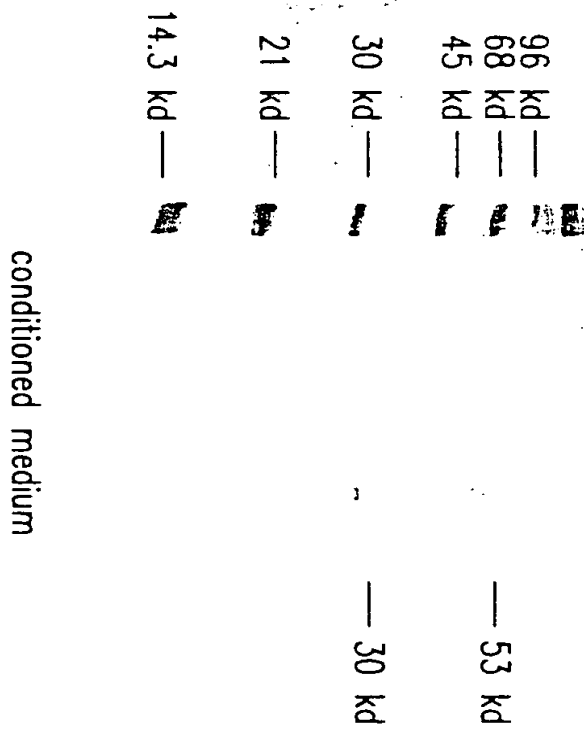
21/47



1. Molecular Weight Marker
2. umbelical vein endothelial cells
3. aortic smooth muscle cells
4. Dermal fibroblast

FIG.15

FIG.16A



1. m.w. marker
2. blank
3. control protein-HA
4. vector control
5. VEGF2-HA

FIG.16B



1. m.w. marker
2. blank
3. control protein-HA
4. VEGF2-HA
5. vector control

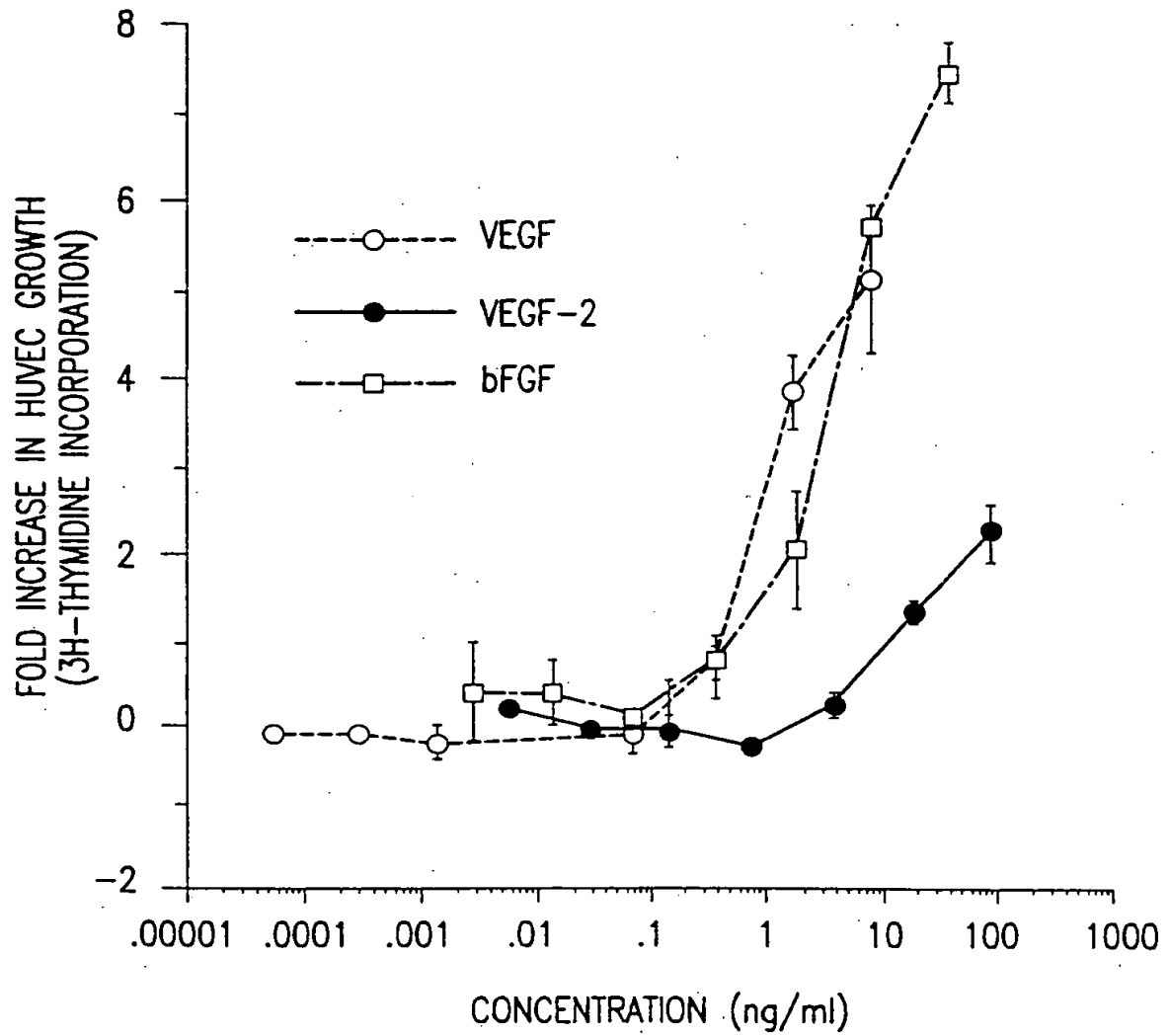


FIG.17

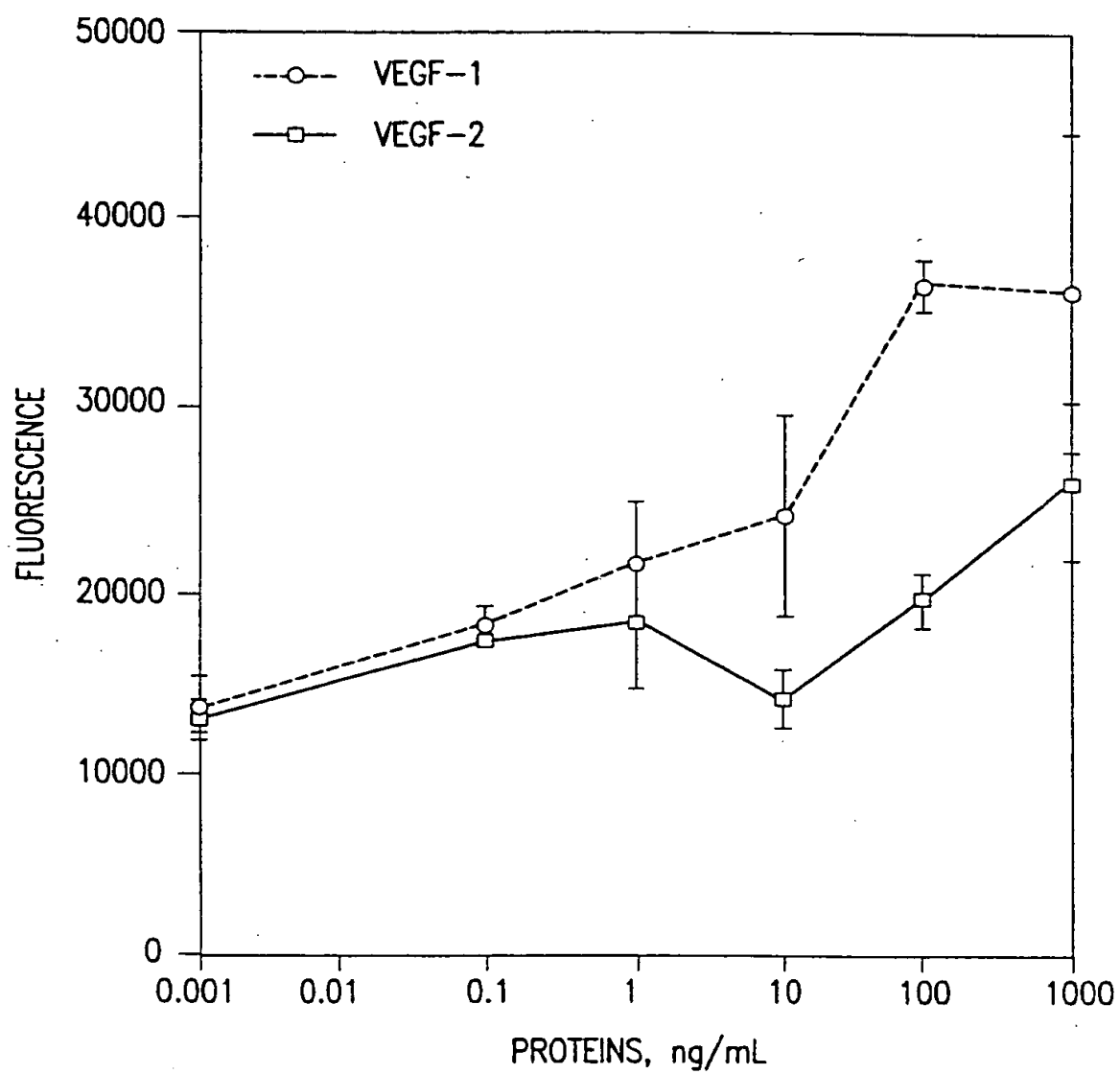


FIG.18

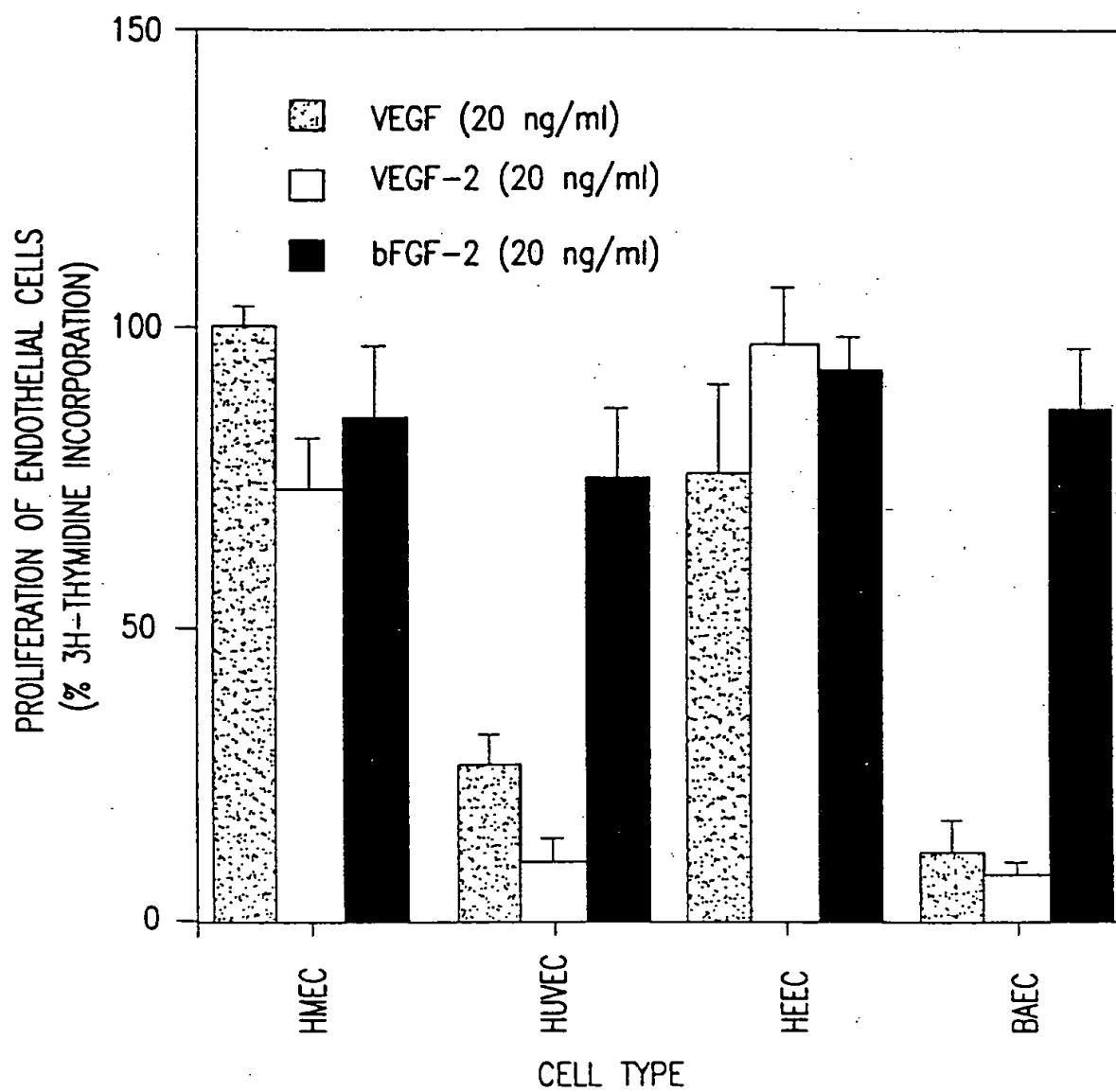


FIG.19

BY [illegible]
[illegible]
[illegible]
[illegible]
[illegible]

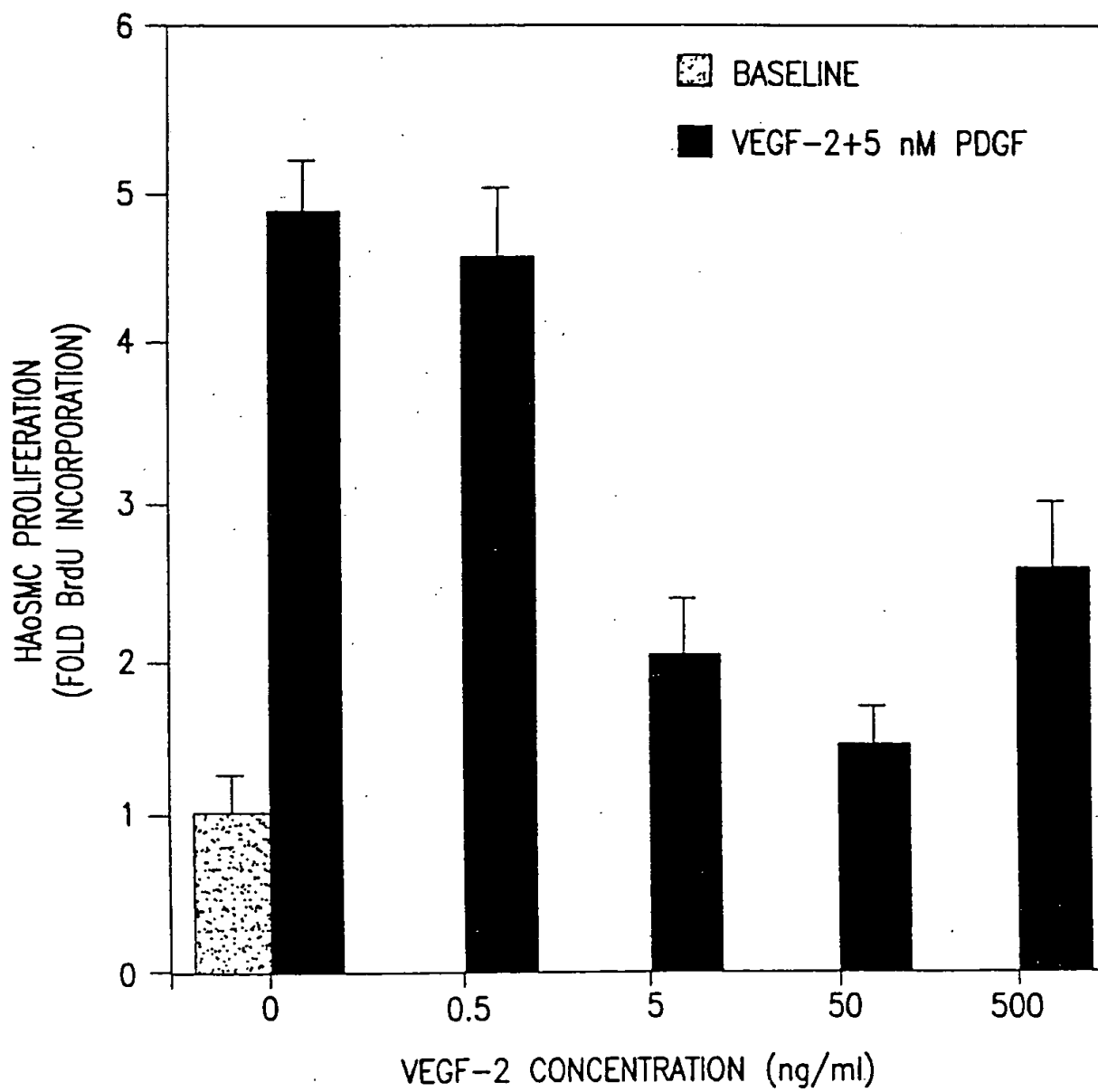


FIG.20A

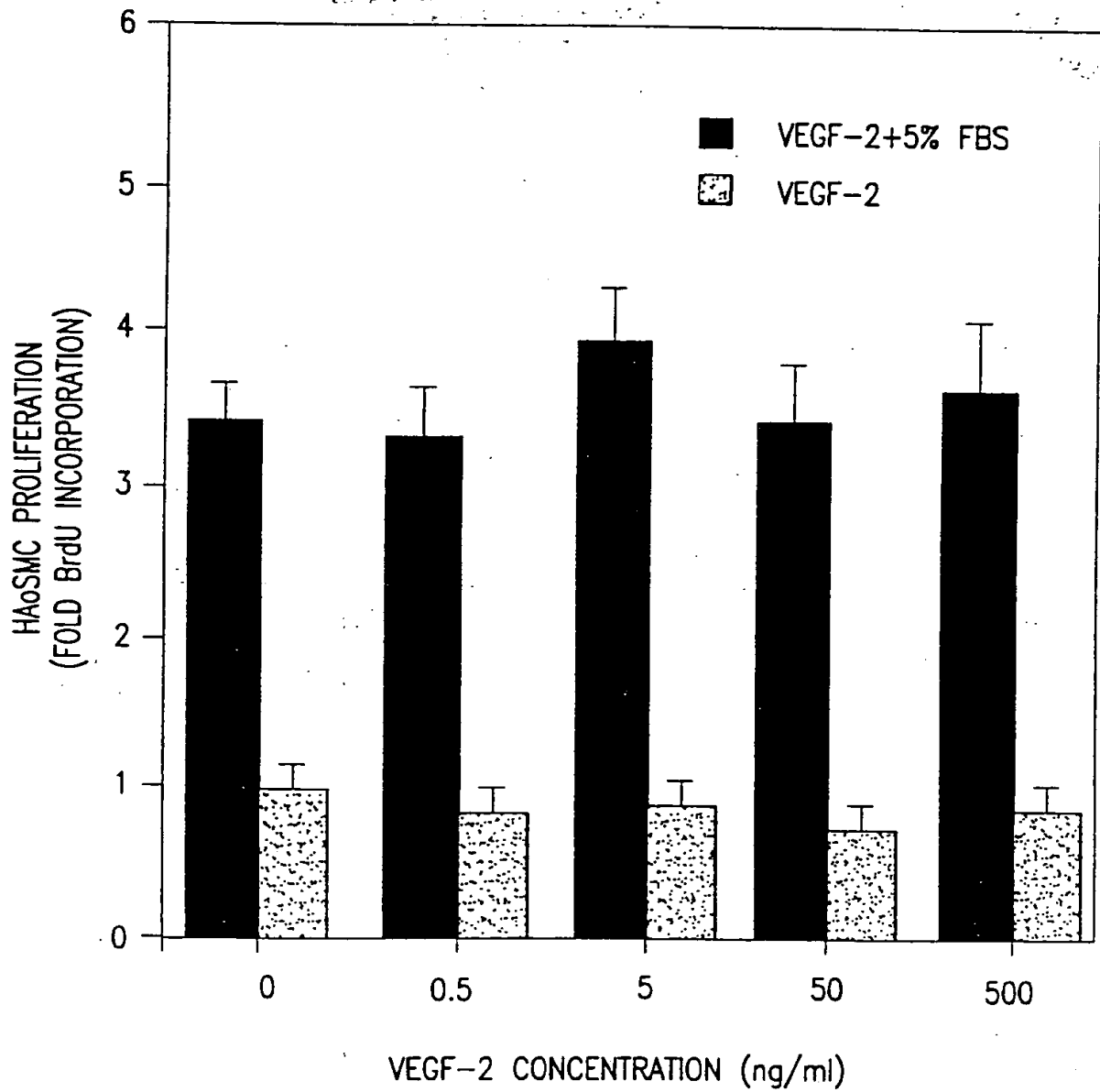


FIG.20B

FIG.21A

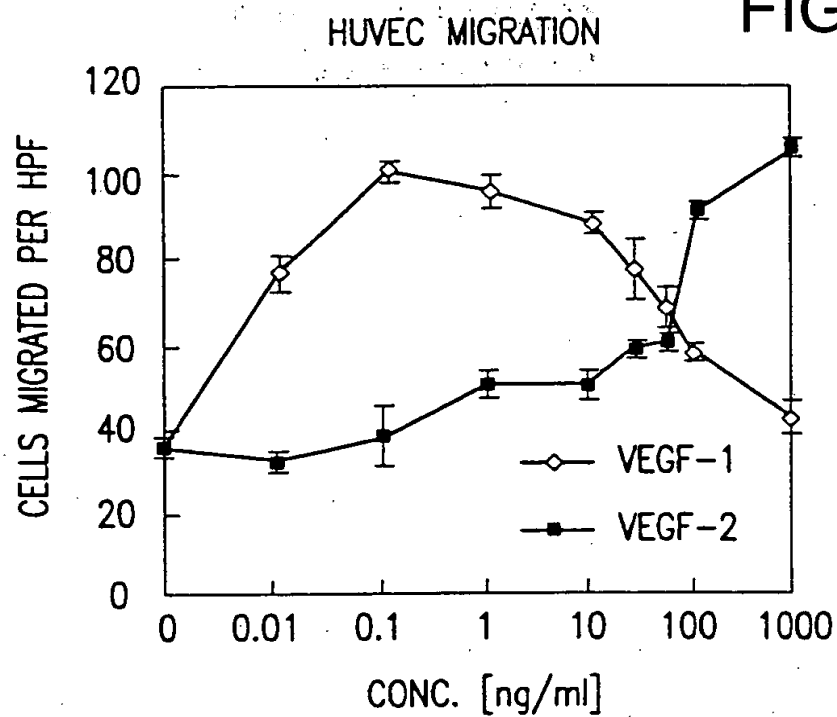
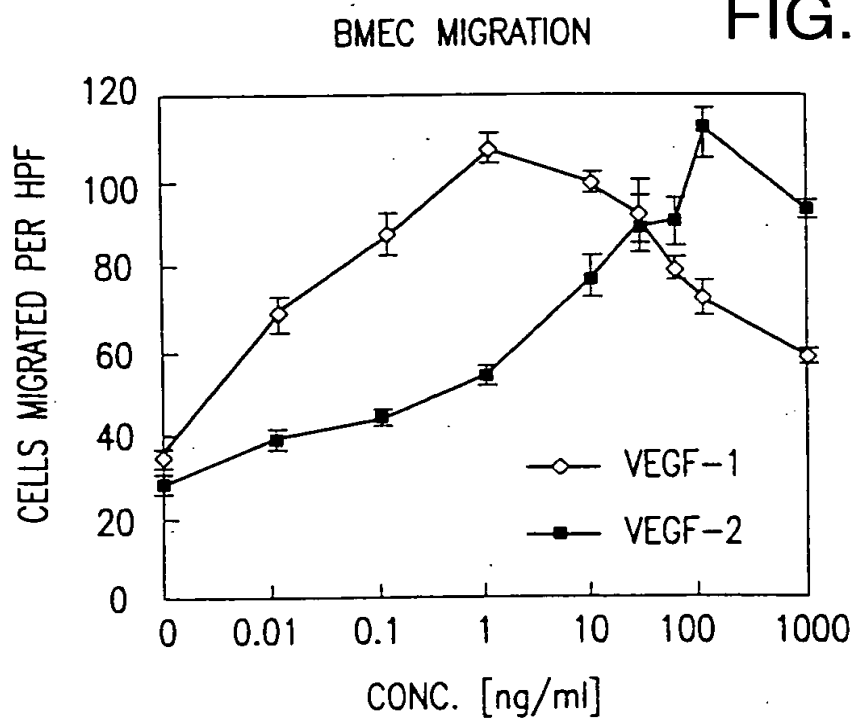


FIG.21B



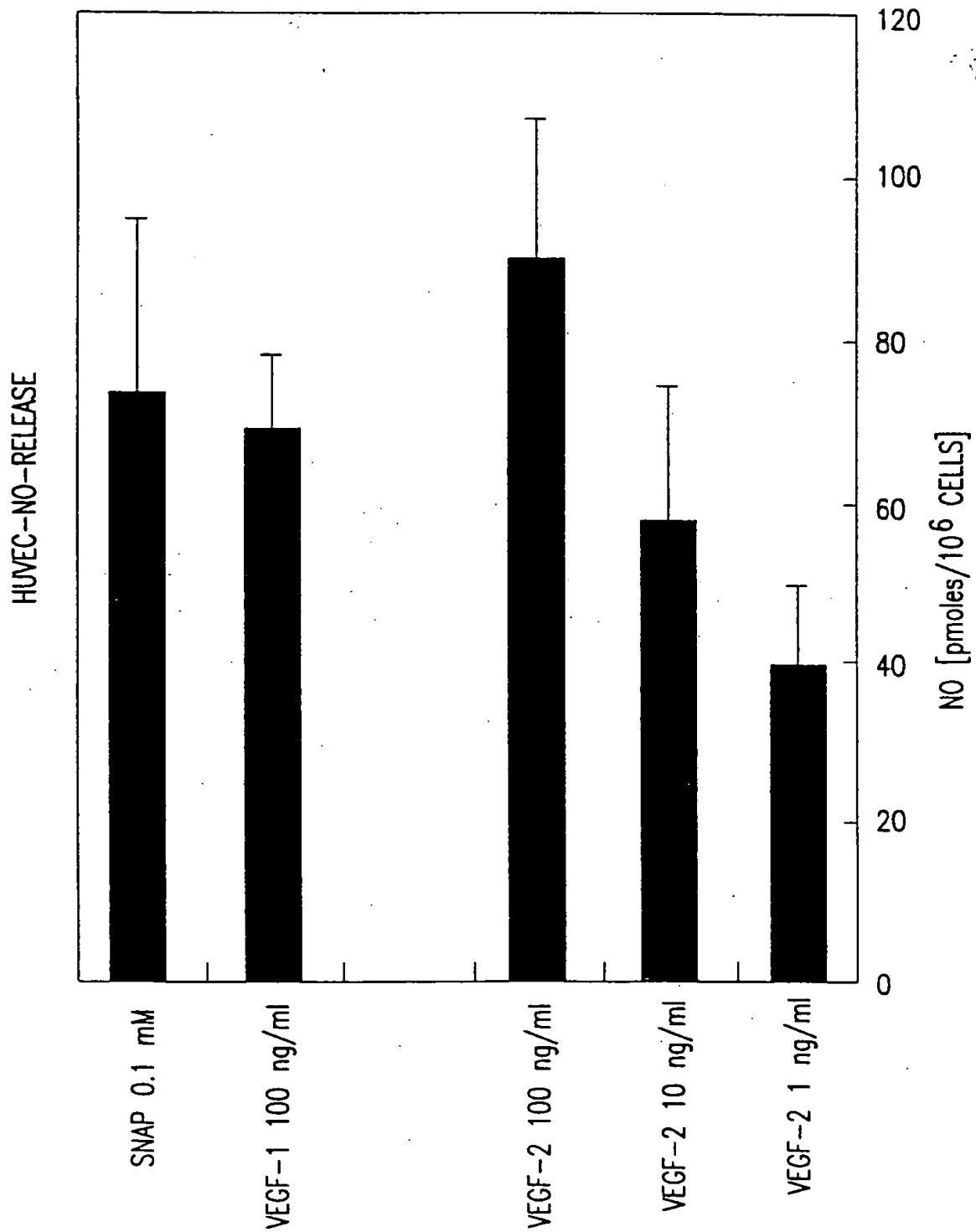


FIG.22

FIG.23

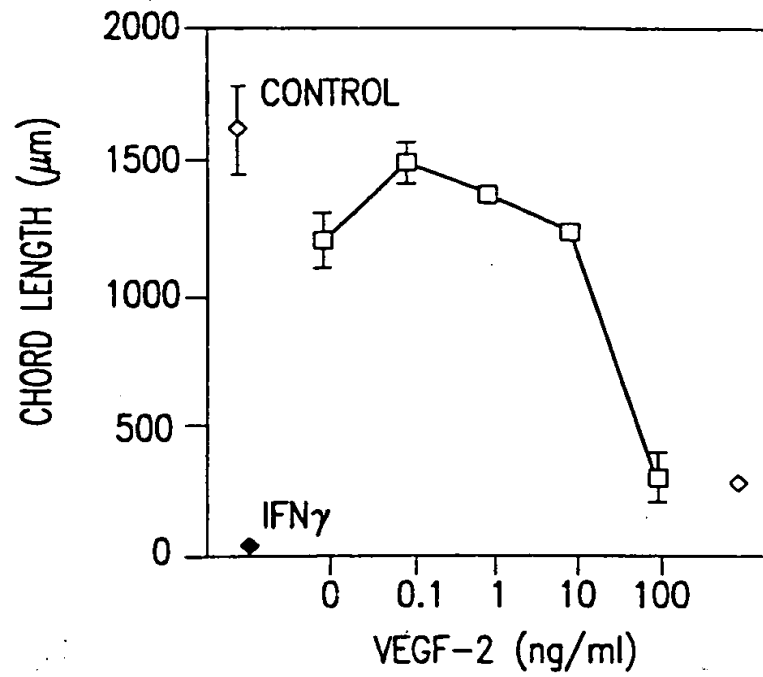


FIG.24

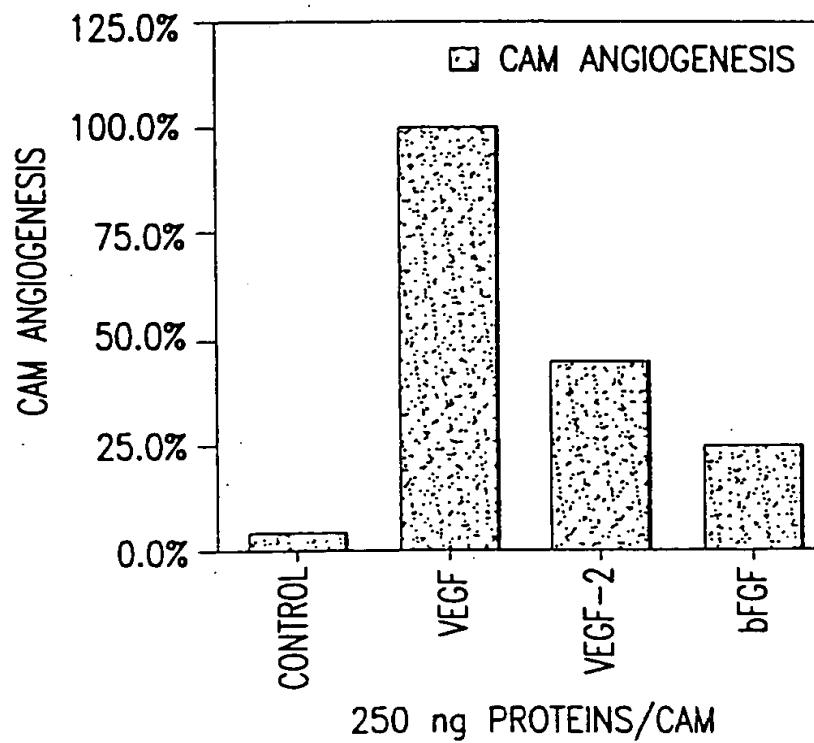


FIG.25A

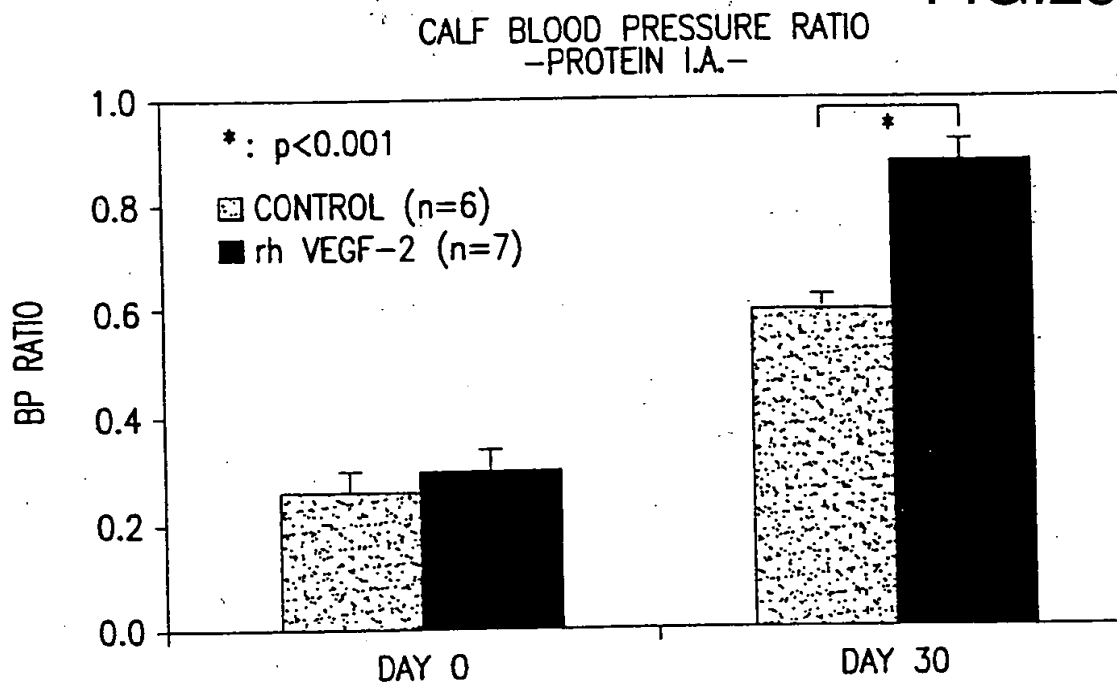
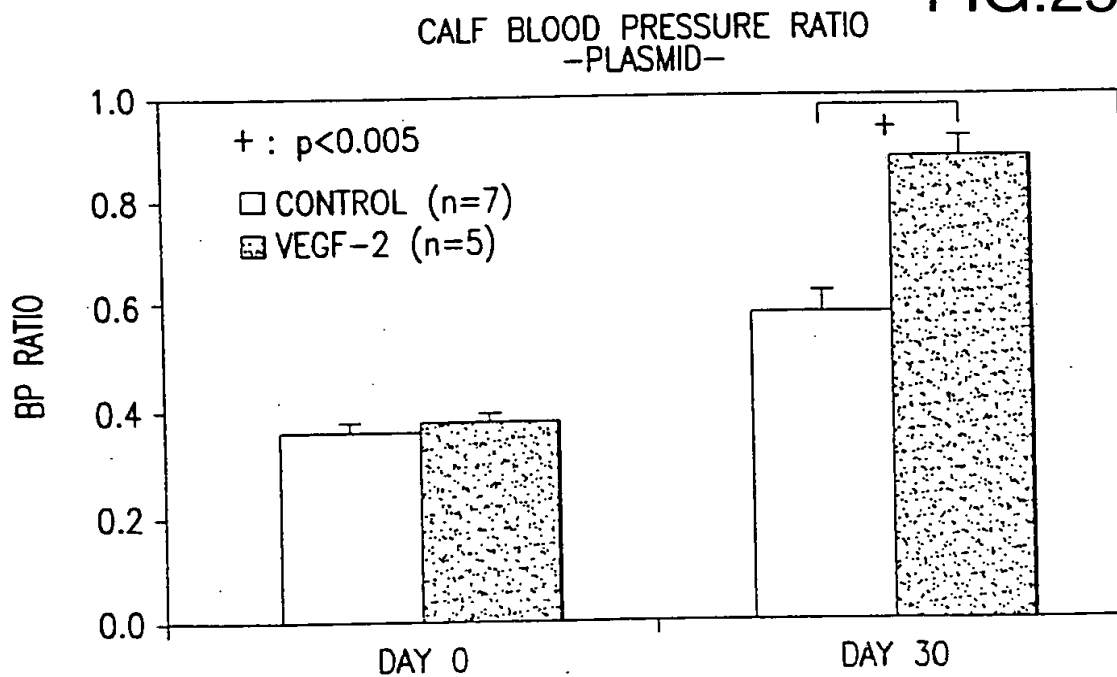


FIG.25B



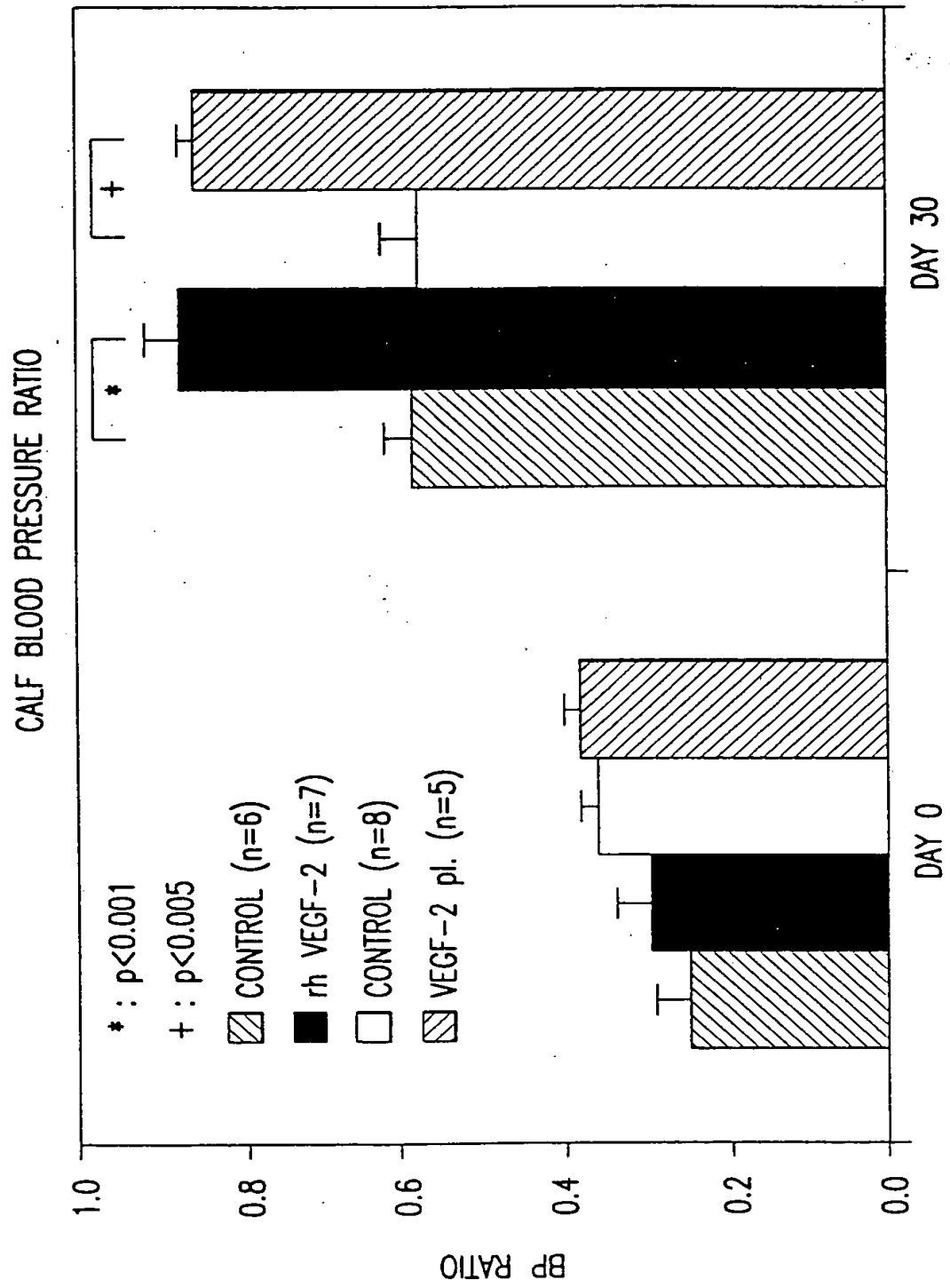
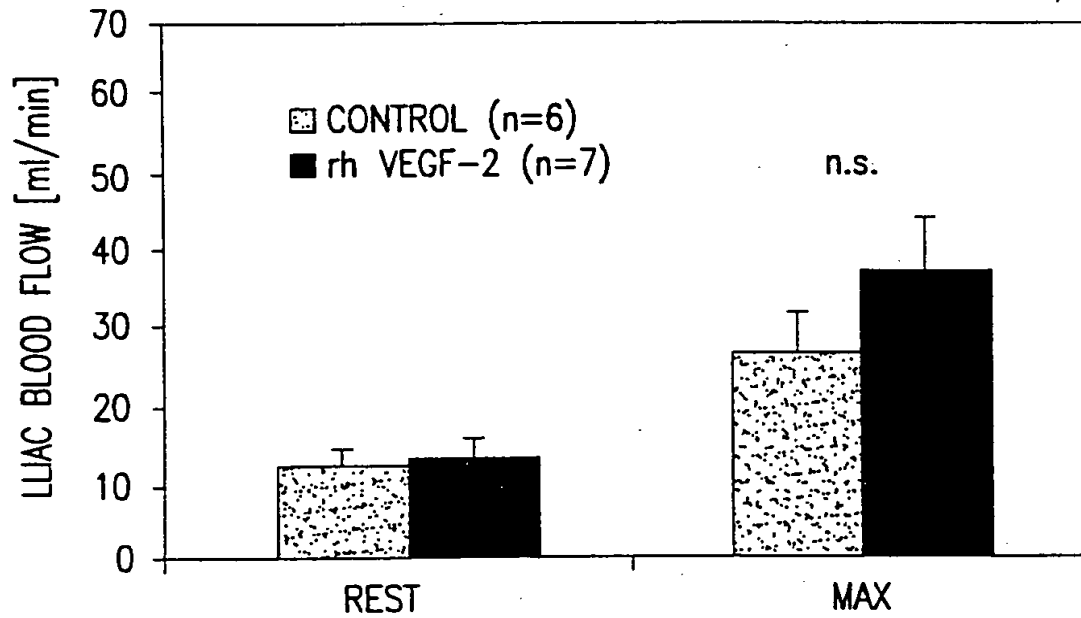


FIG.25C

33/47

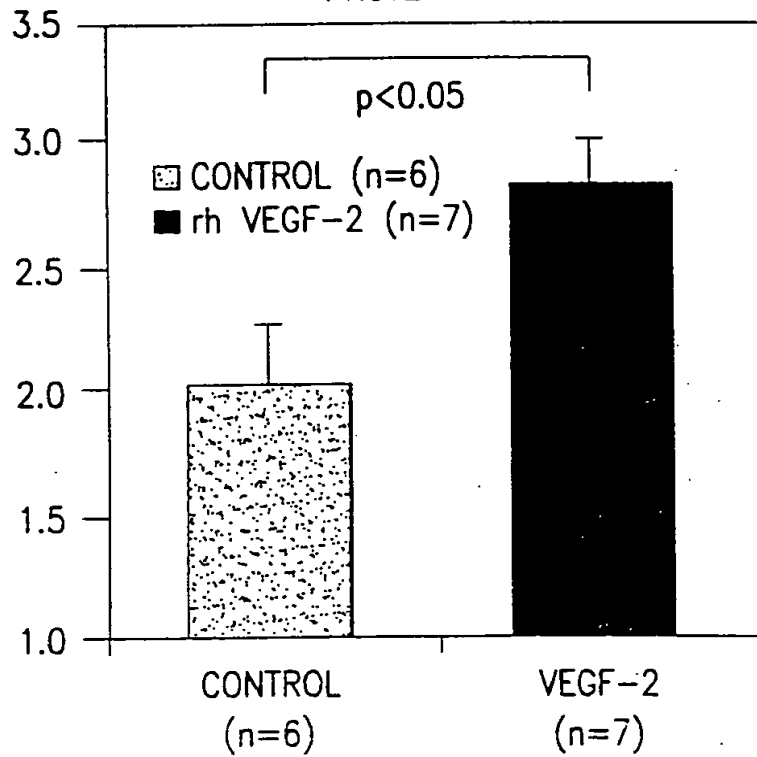
LLIAC BLOOD FLOW
-PROTEIN I.A.-

FIG.25D



LLIAC FLOW RESERVE
-PROTEIN I.A.-

FIG.25E



LLIAC BLOOD FLOW
-PLASMID-

FIG.25F

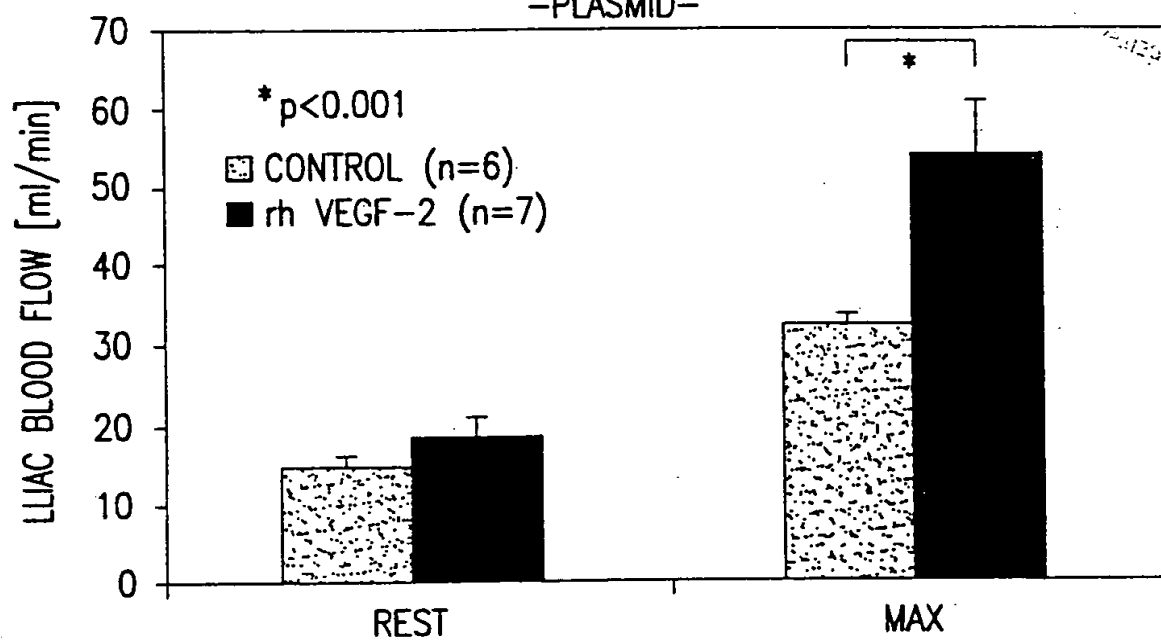
LLIAC FLOW RESERVE
-PLASMID-

FIG.25G

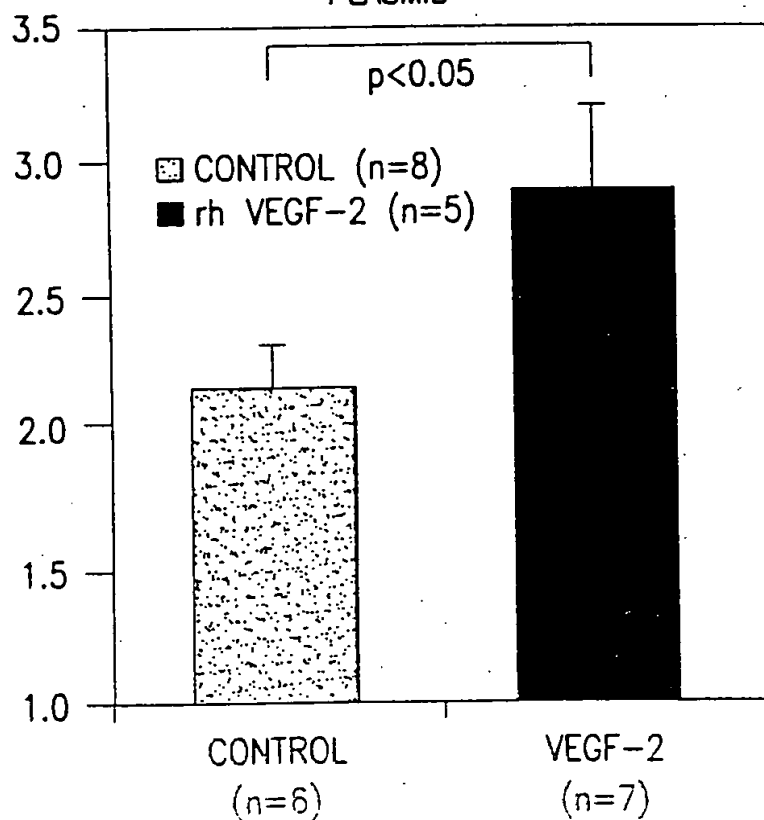


FIG.25H

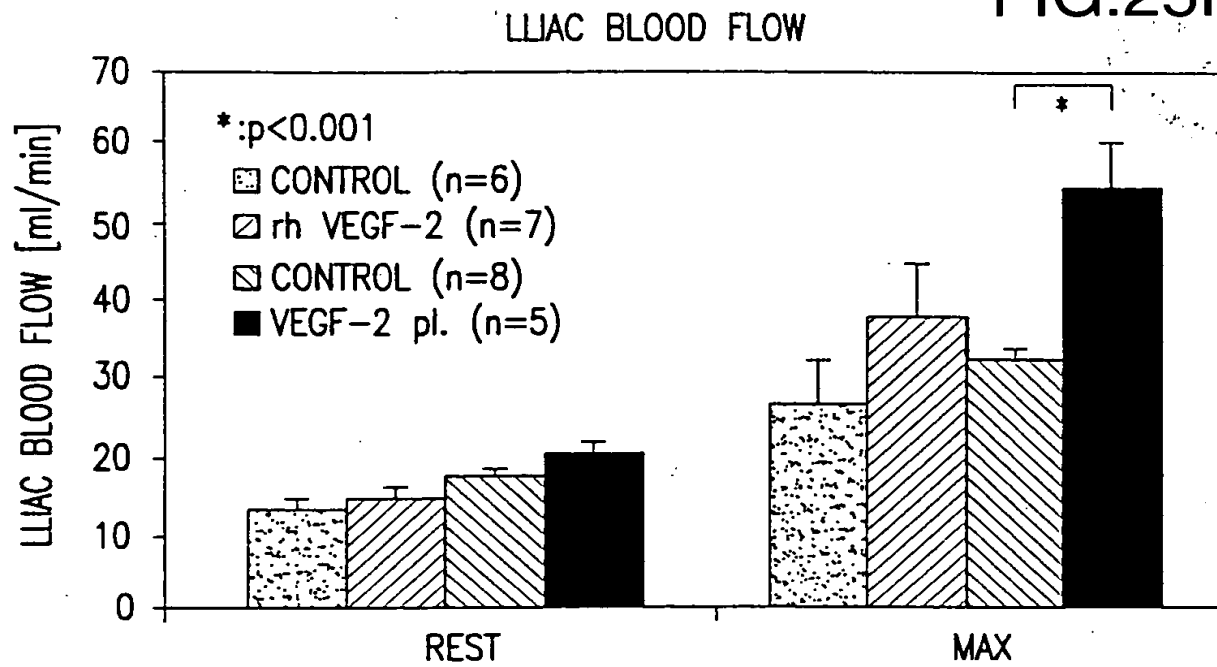
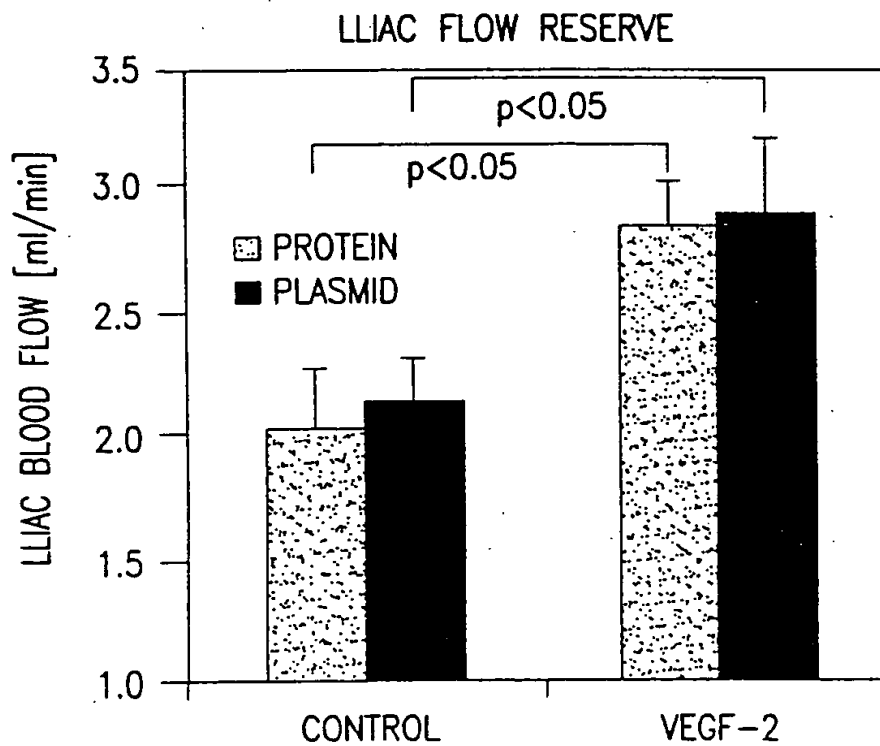


FIG.25I



ANGIOGRAPHIC SCORE
-PROTEIN I.A.-

FIG.25J

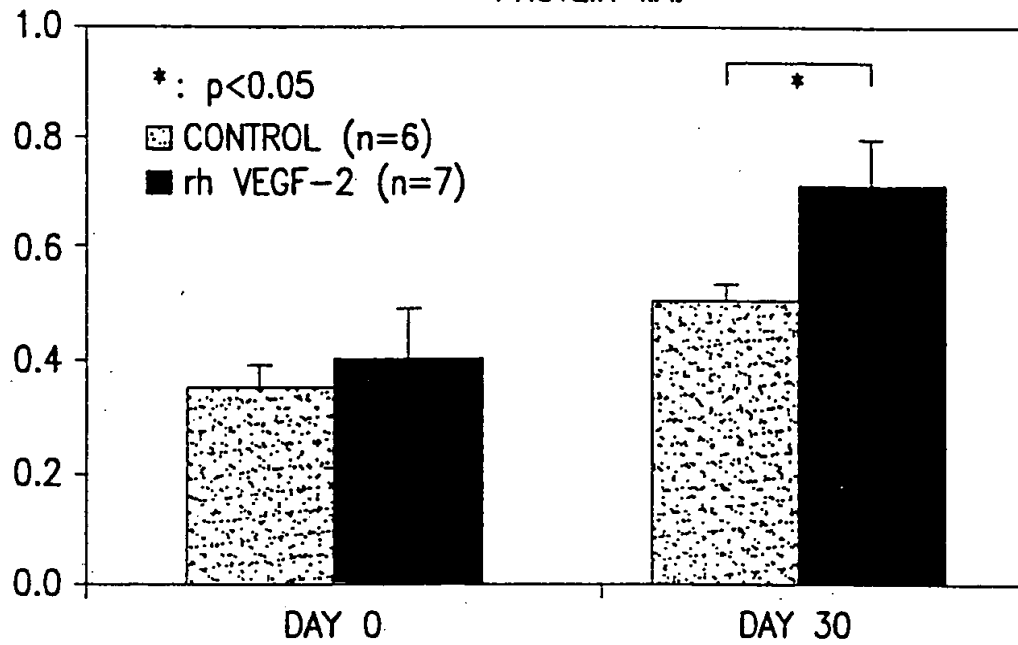
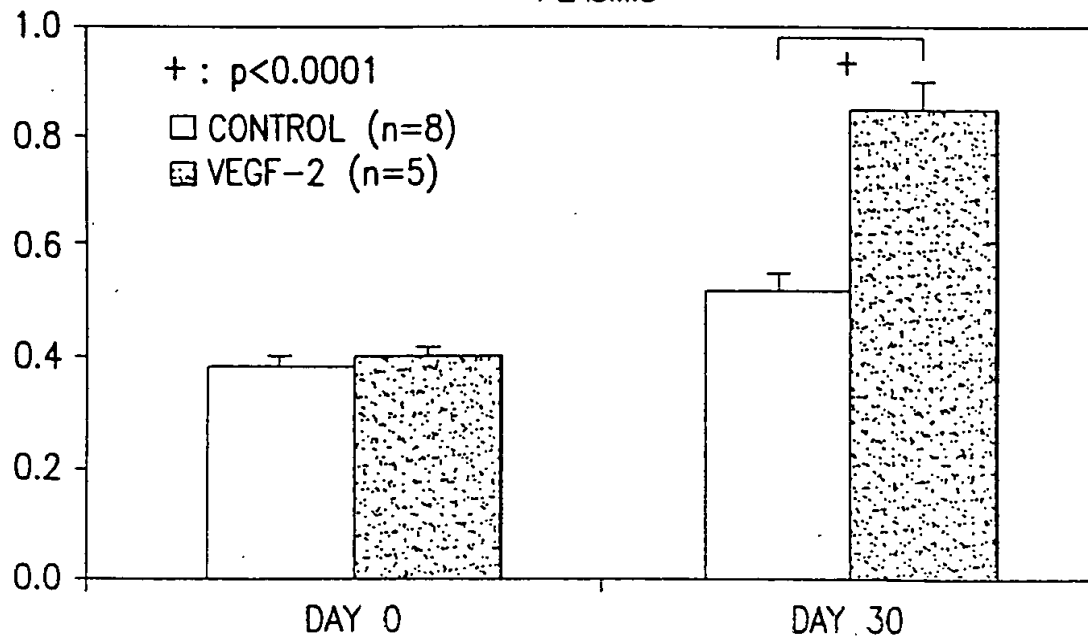
ANGIOGRAPHIC SCORE
-PLASMID-

FIG.25K



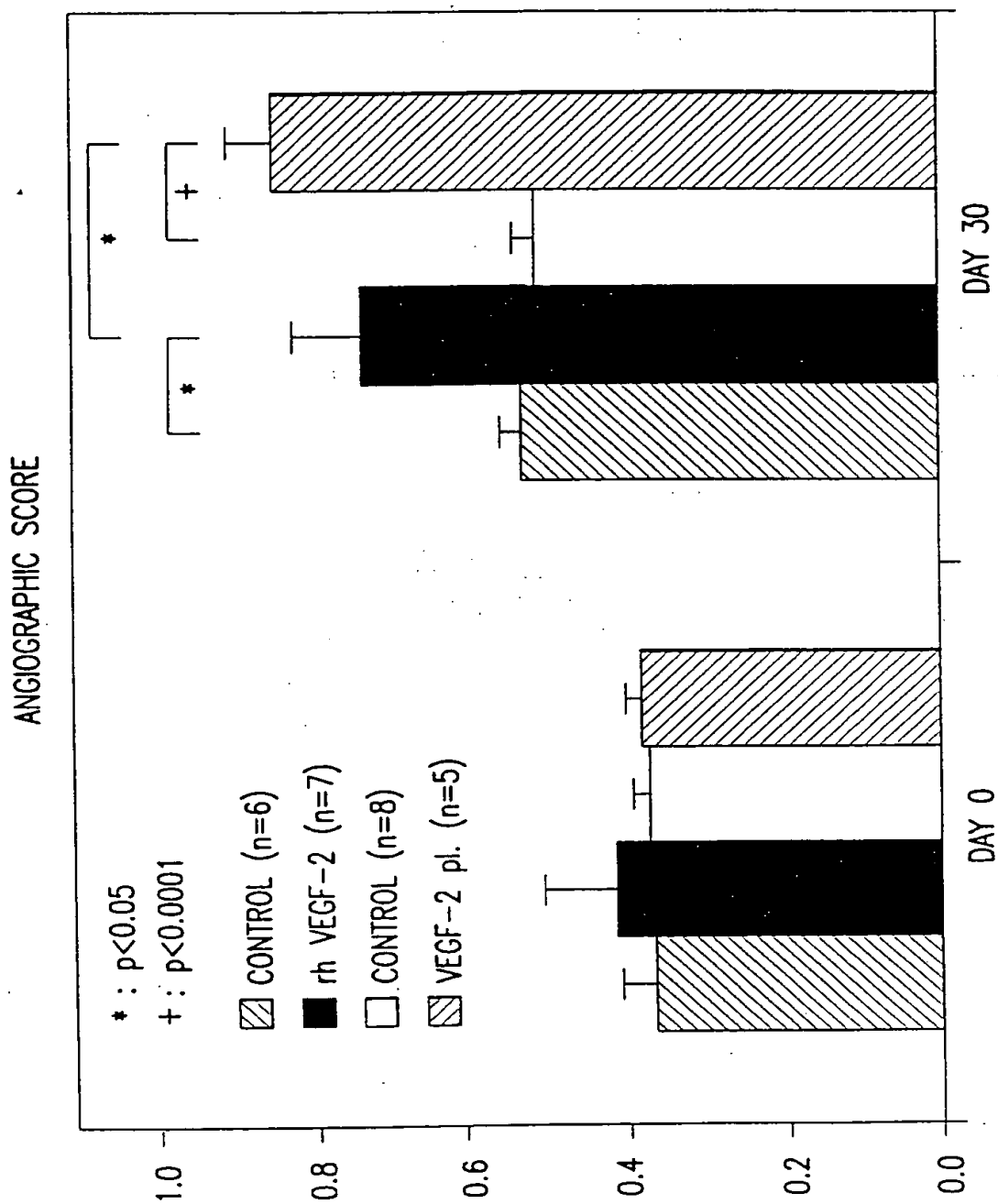


FIG.25L

38/47

FIG.25M

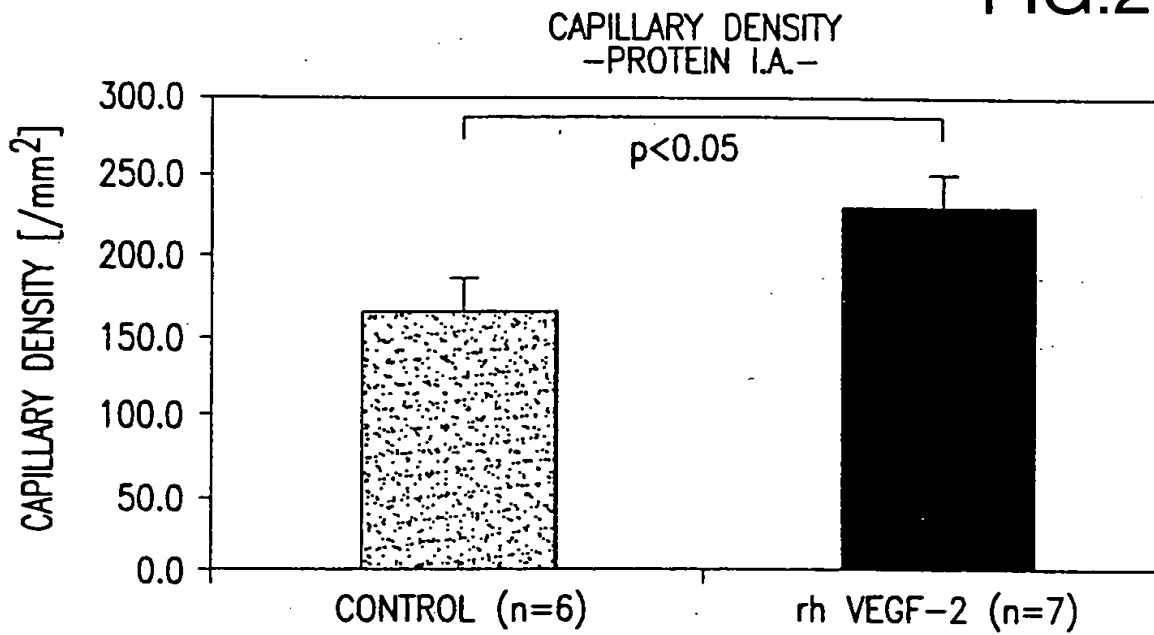
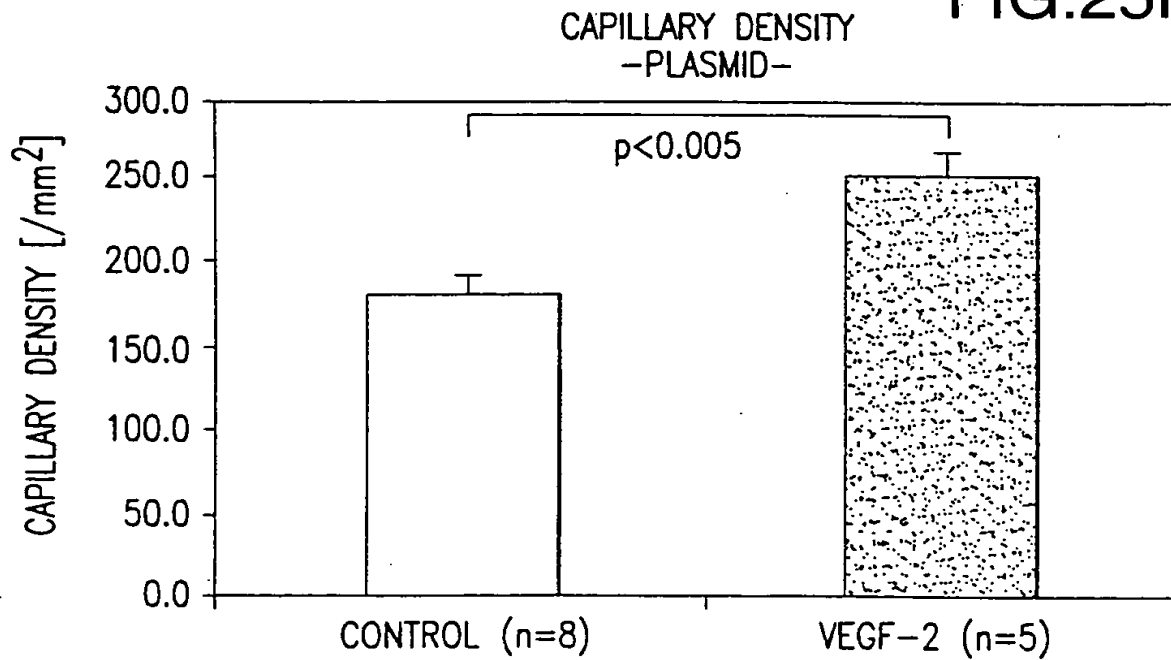


FIG.25N



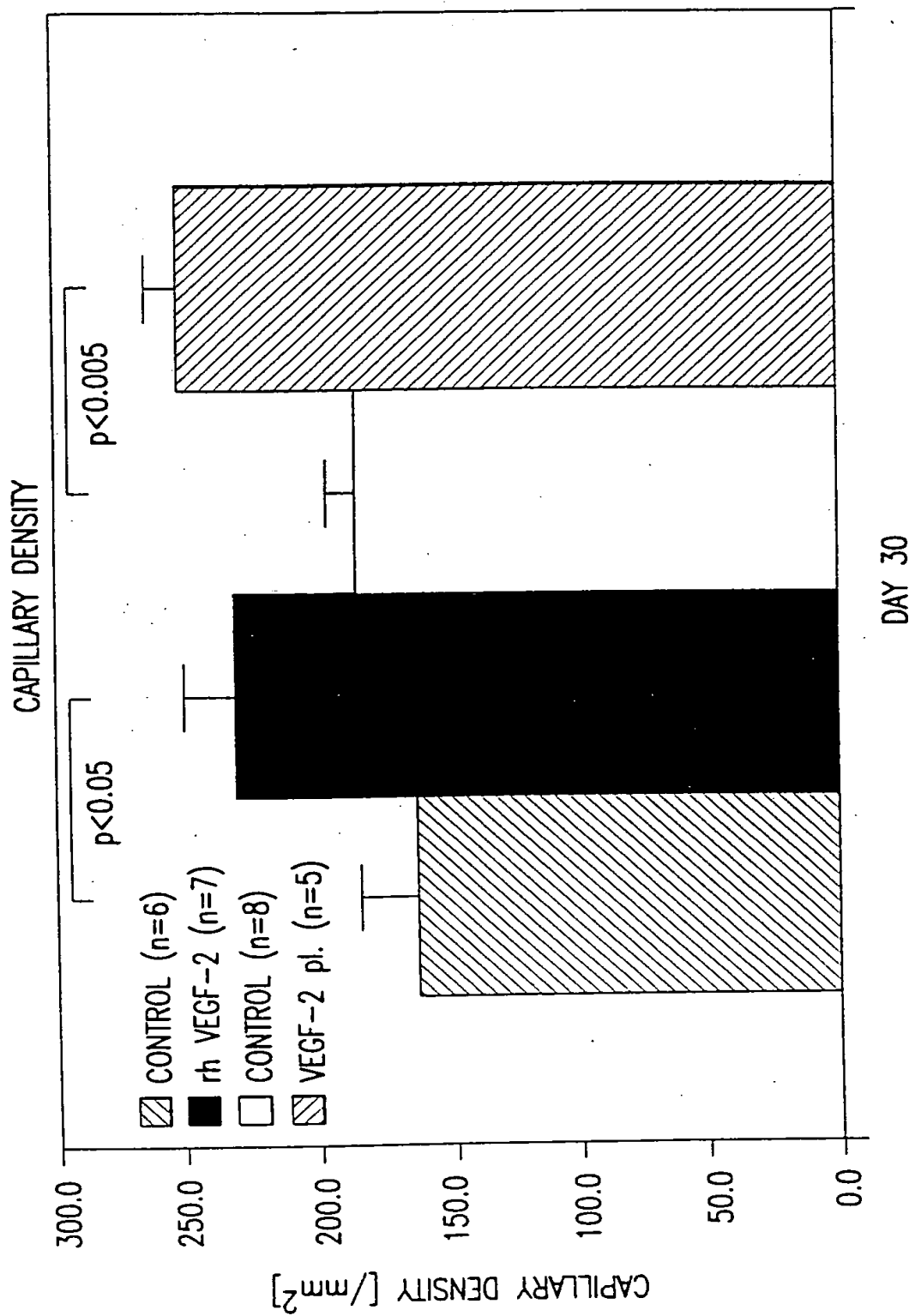


FIG.250

40/47

FIG.26A

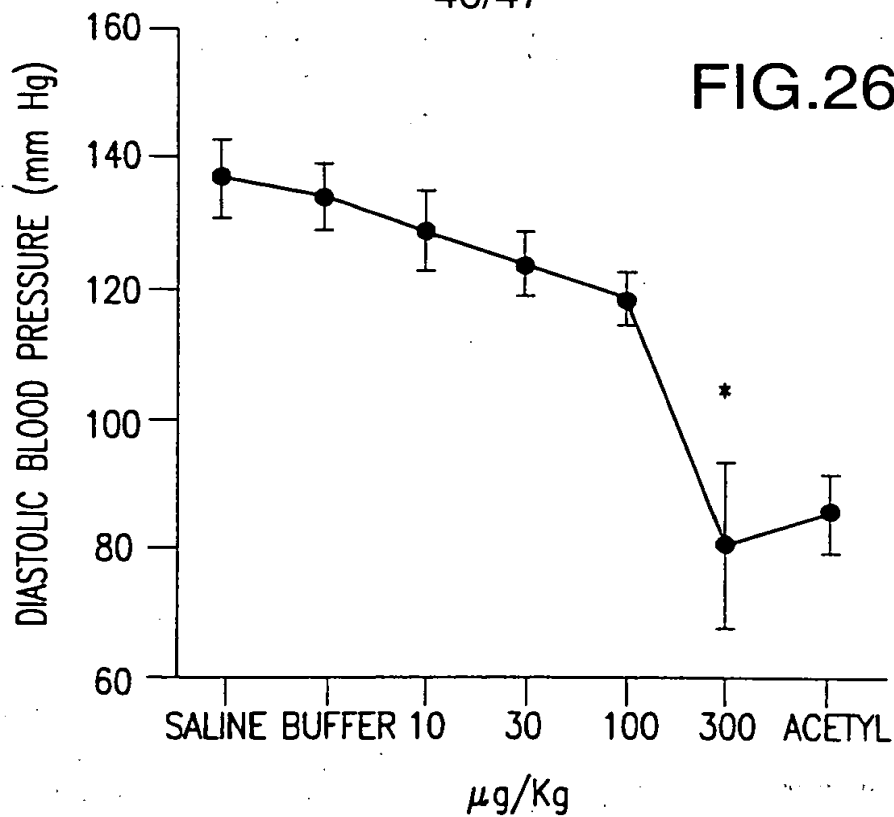
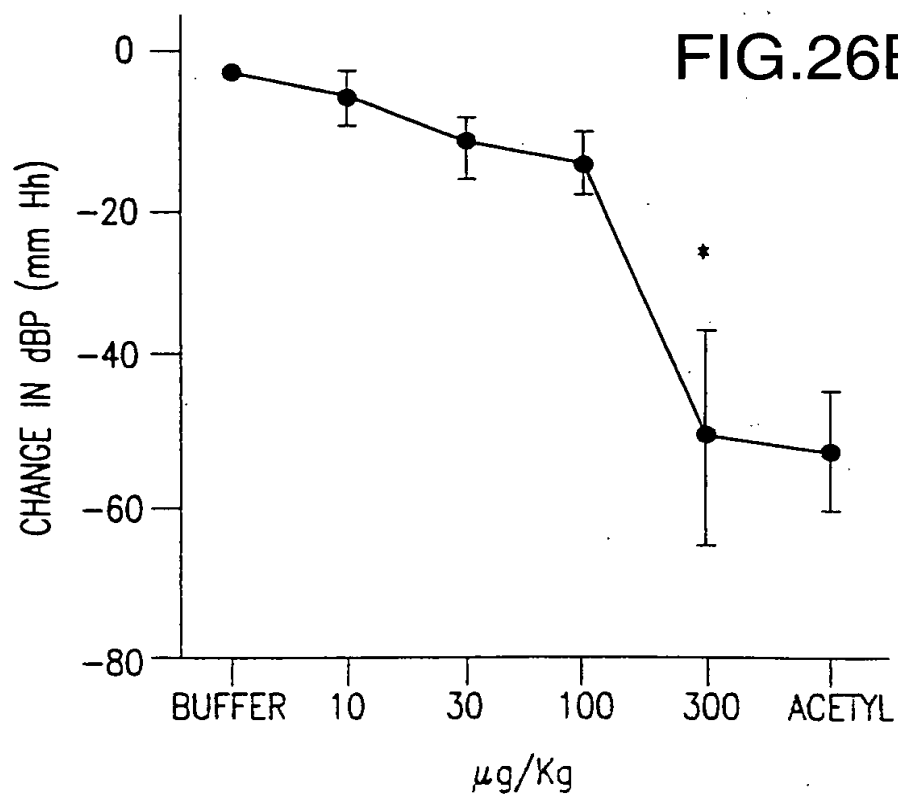


FIG.26B



2025-09-22 09:00

41/47

FIG.26C

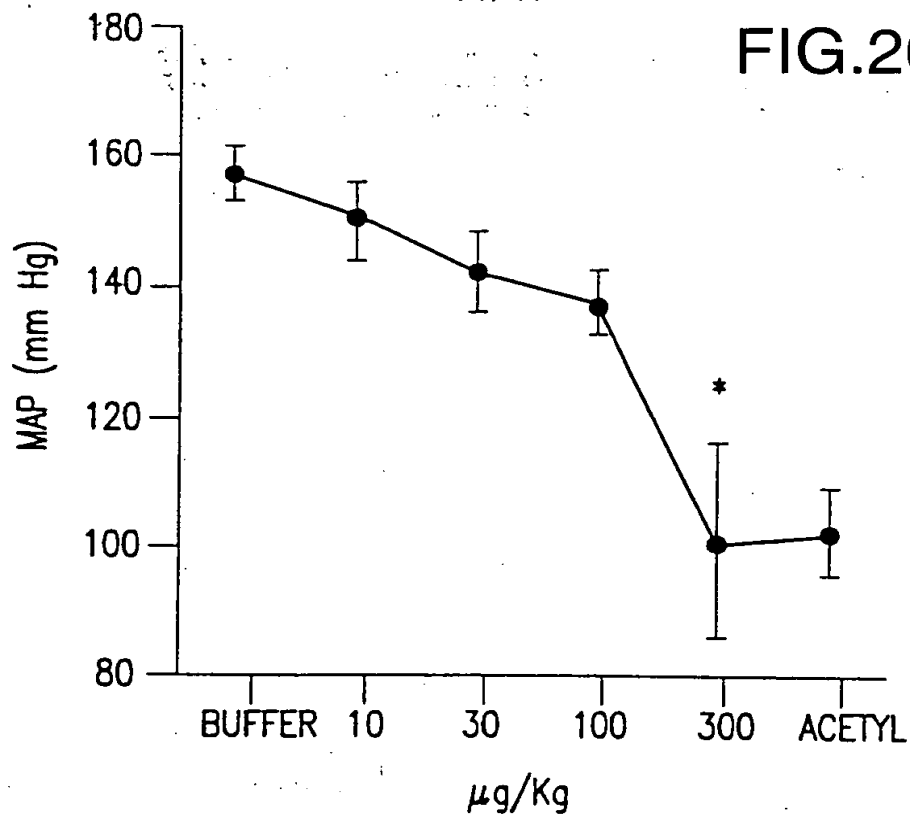
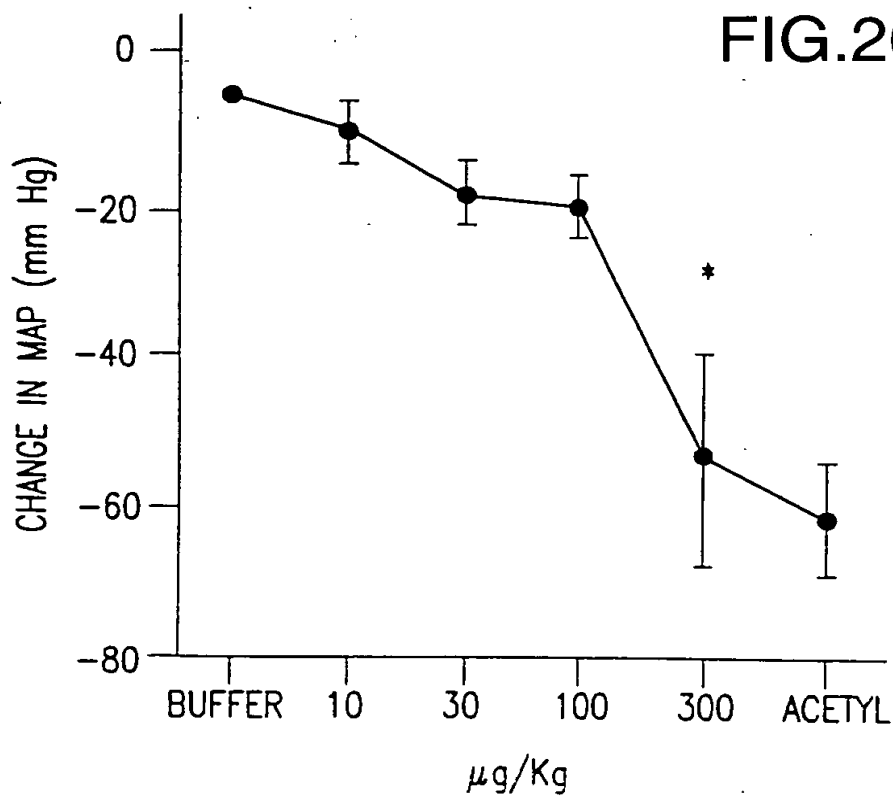


FIG.26D



CHANGE IN DIASTOLIC BLOOD PRESSURE OF SHR RATS GIVEN
INCREASING DOSES OF VEGF-2

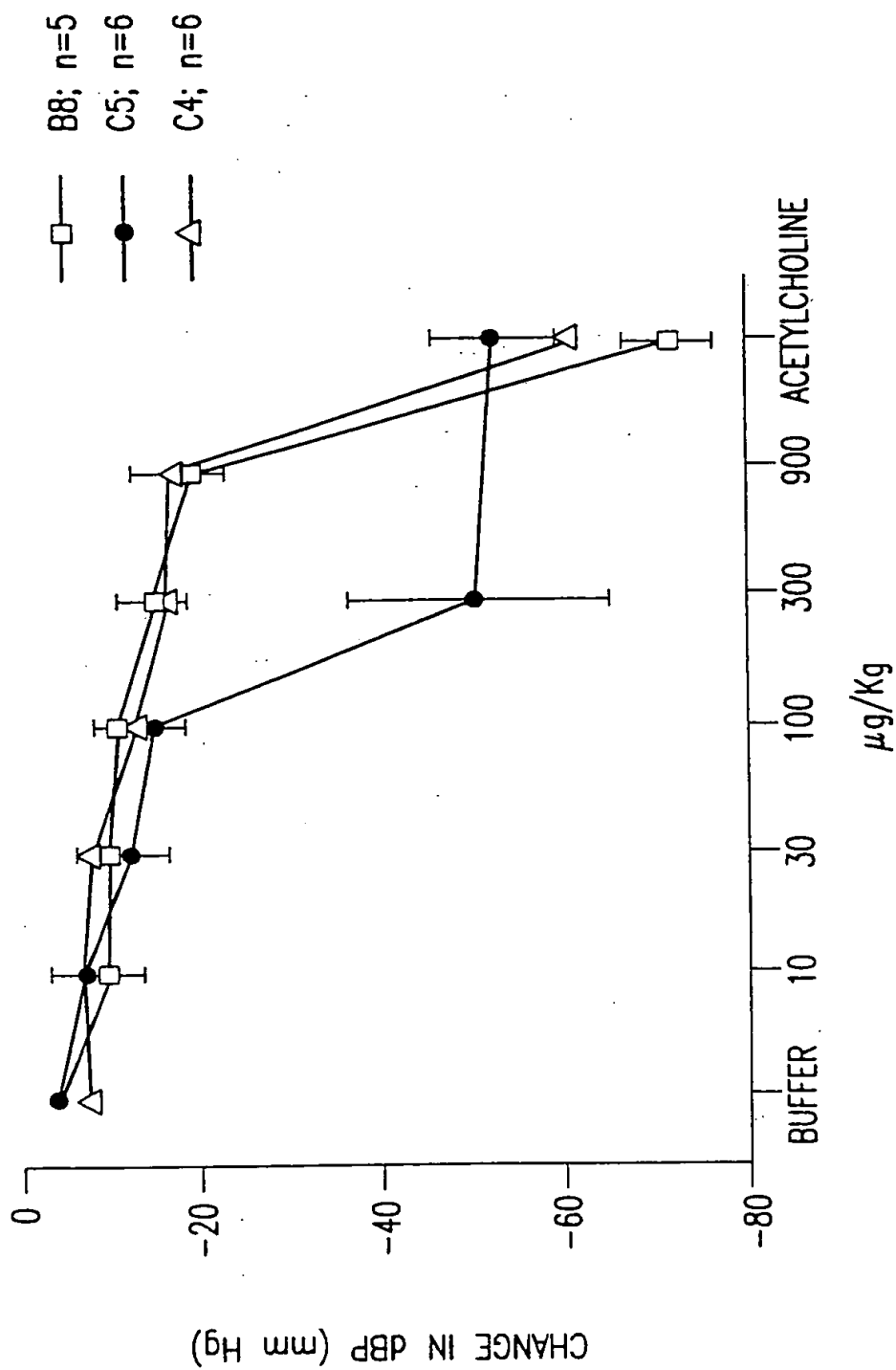


FIG.26E

THE EFFECT OF INCREASING DOSES OF VEGF-2 ON THE
MEAN ARTERIAL PRESSURE (MAP) OF SHR RATS

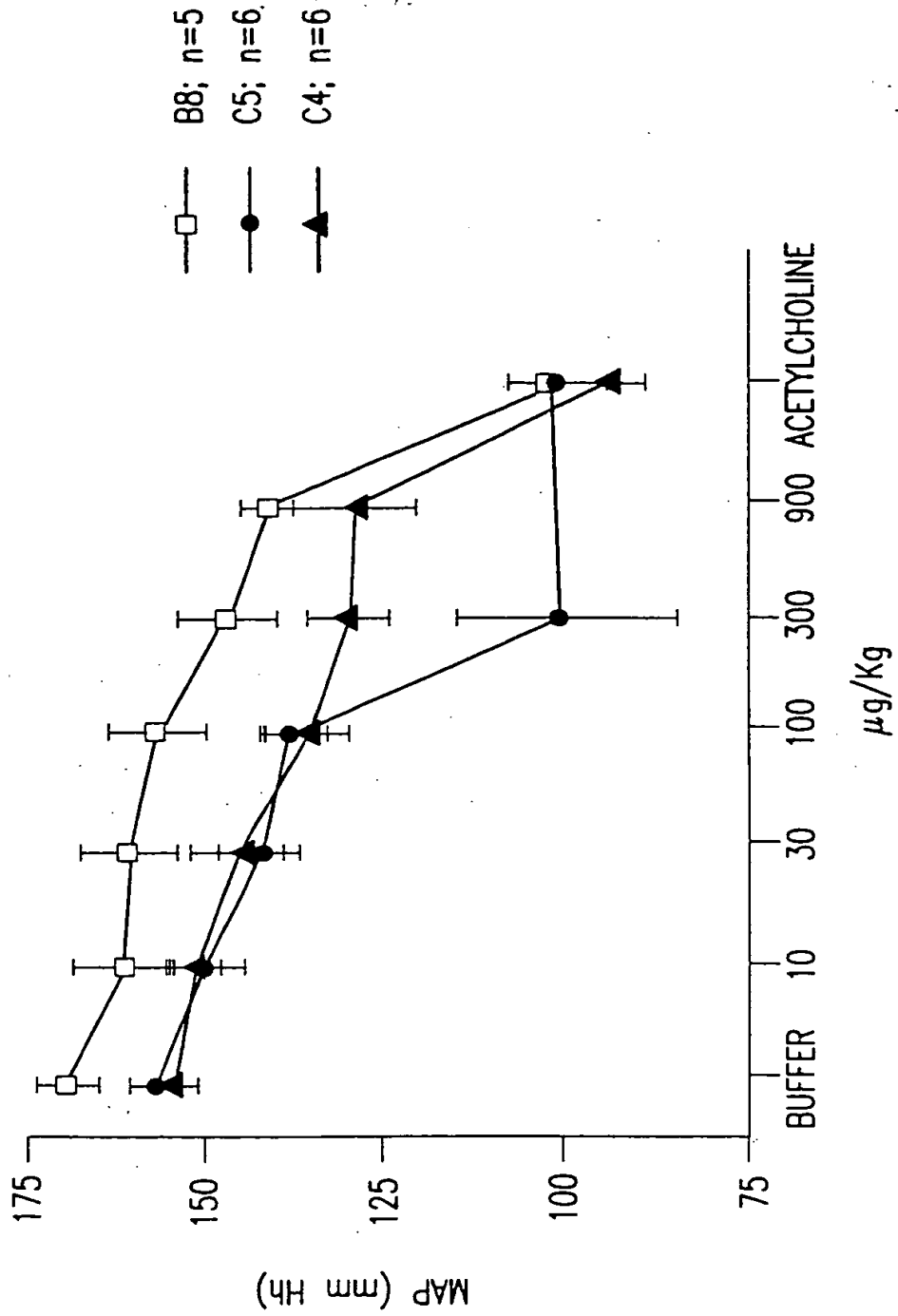


FIG.26F

THE EFFECT OF VEGF-2 ON THE DIASTOLIC BLOOD PRESSURE OF SHR RATS

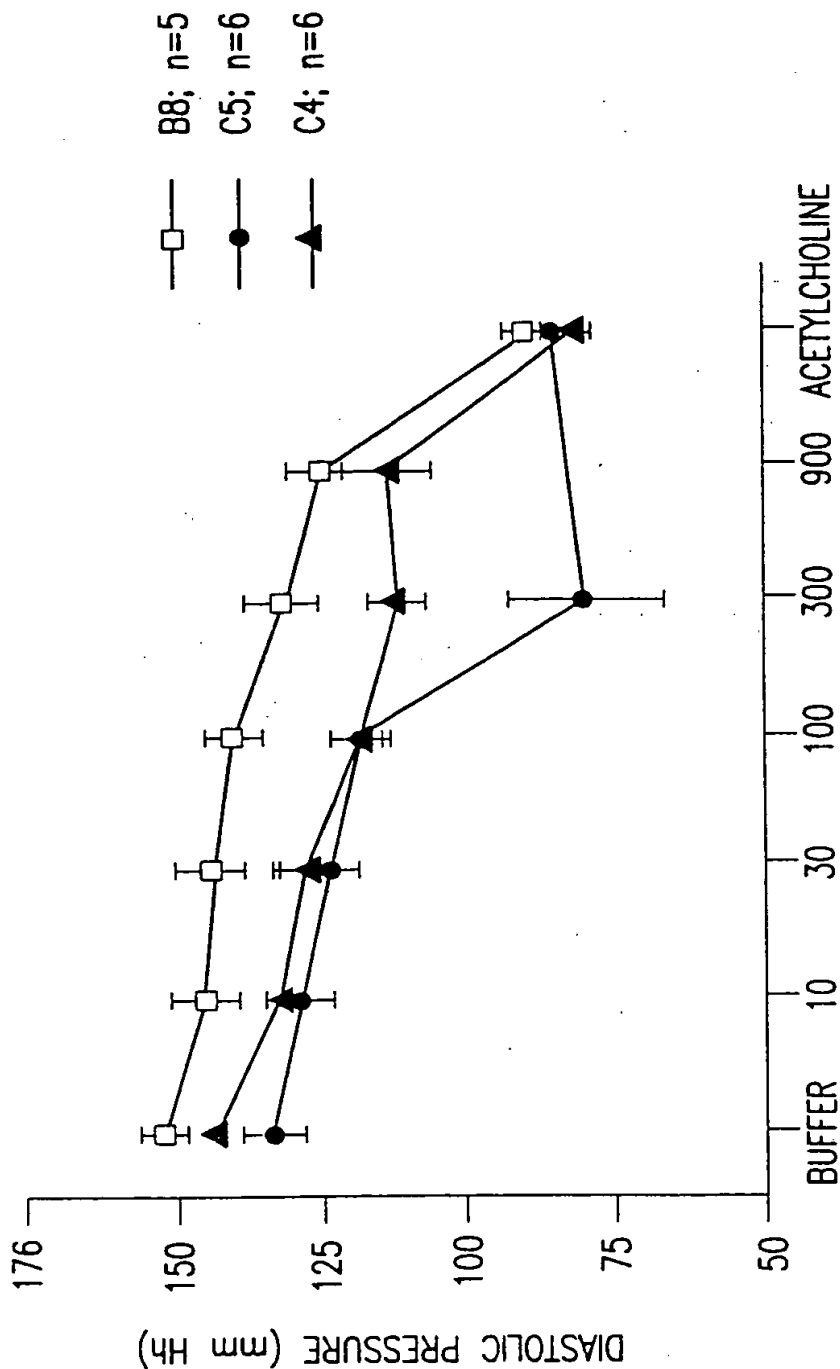


FIG.26G

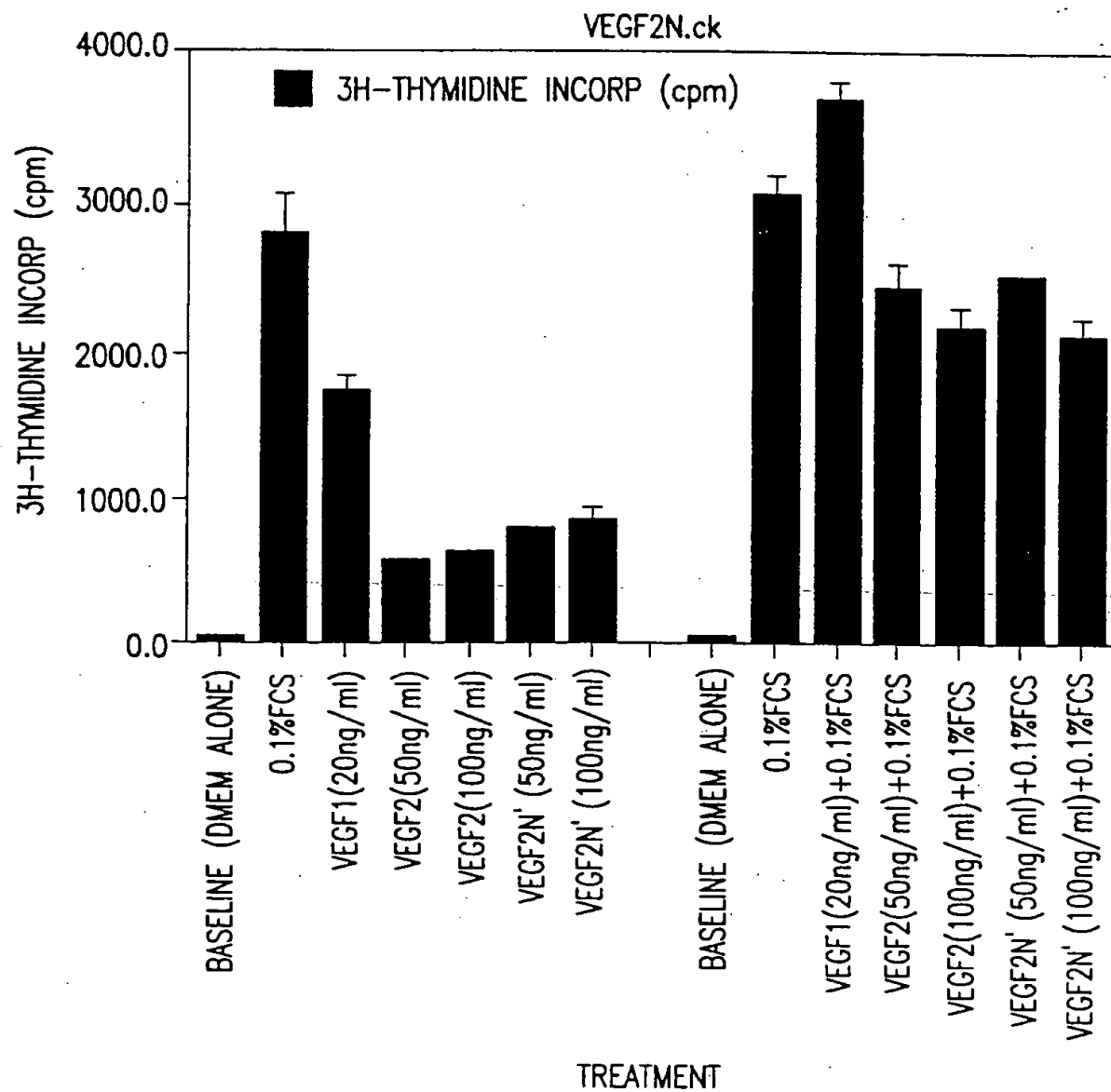


FIG.27

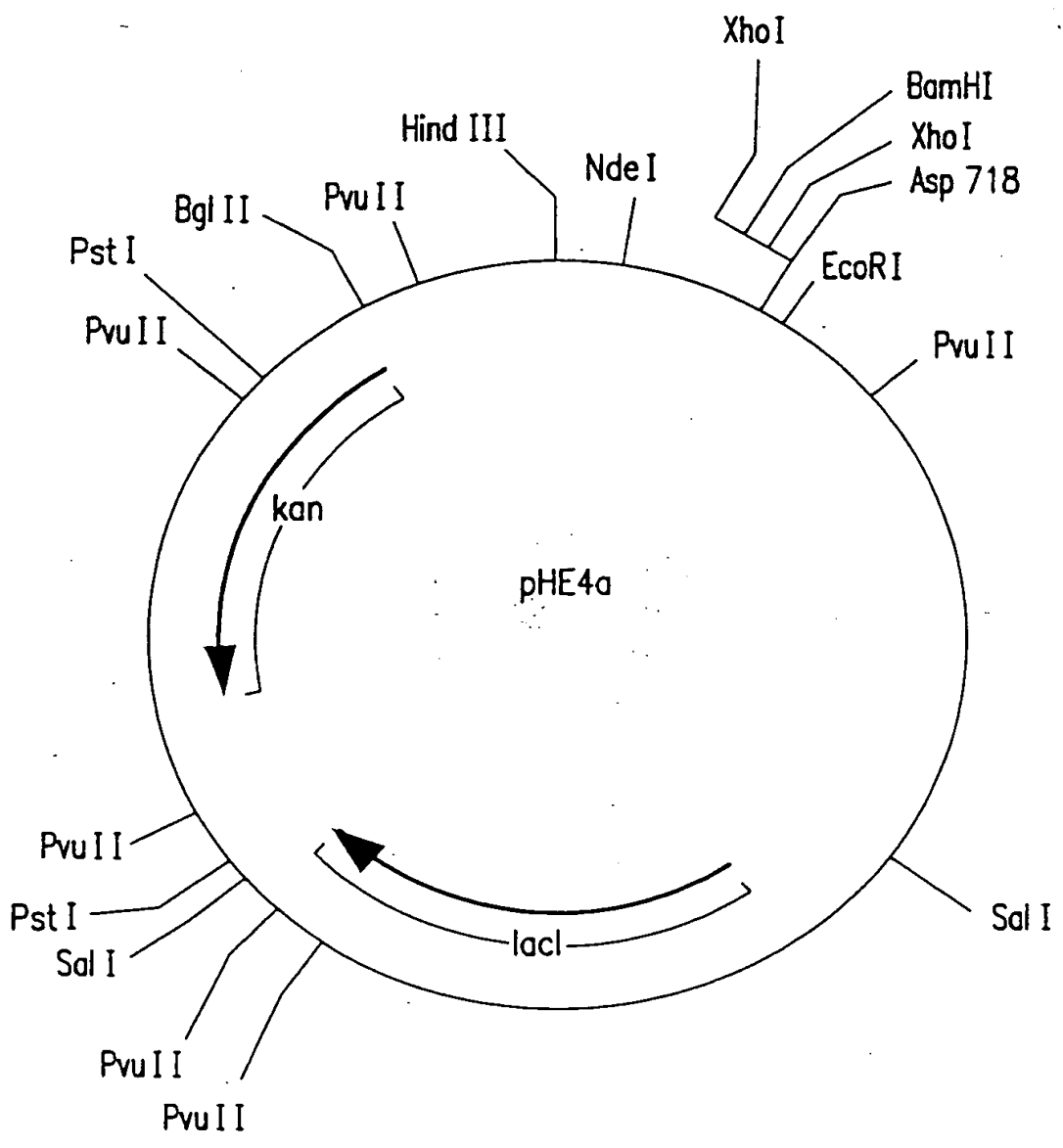


FIG.28

202210-9275200

205210-9245550

OPERATOR 1

-35

1 AAGCTTAACTGCAAAATAGTTTGACTTGTGAGCGGATAACAAT

OPERATOR 2

-10

50 TAAGATGTACCCCAATTGTGAGCGGATAACAATTTCACACATTAA

S/D

94 AGAGGAGAAATTA CATATG

47/47

FIG.29